

FIGURE 1A



FIGURE 1B

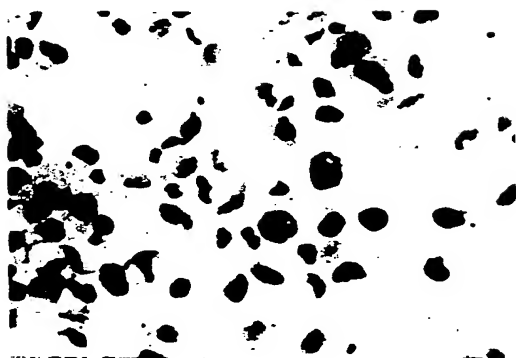


FIGURE 1C



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FIGURE 2

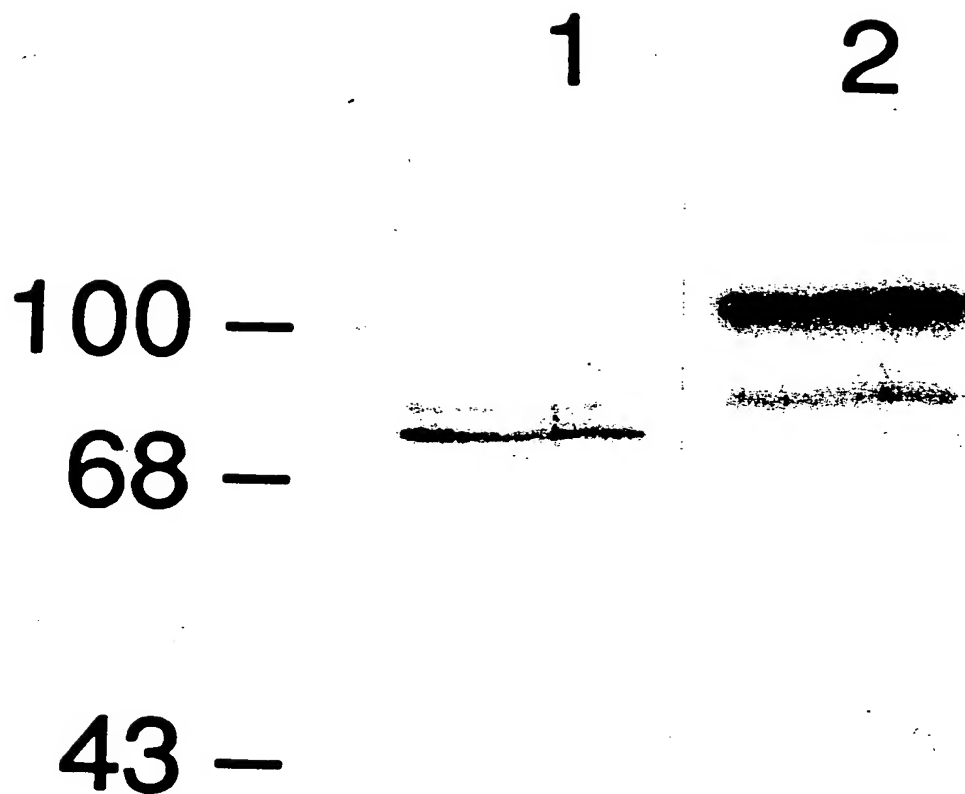
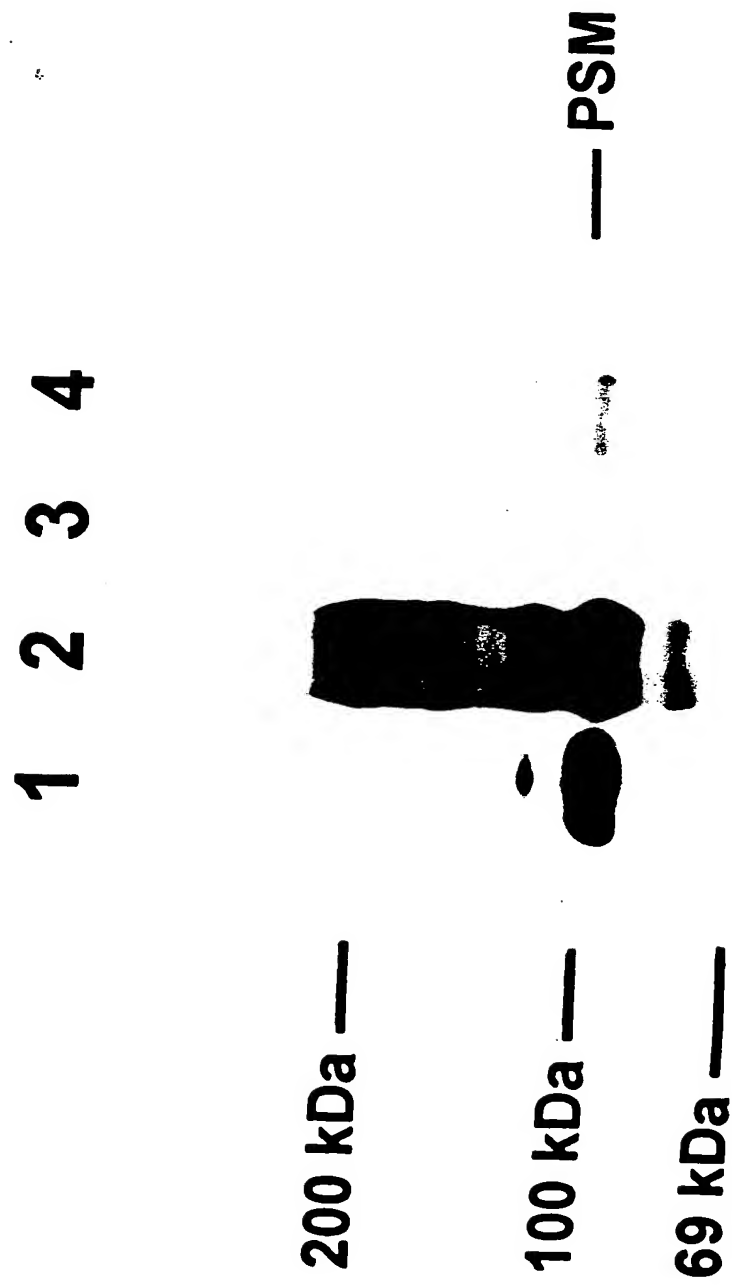


FIGURE 3



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350

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

400

FIGURE 4

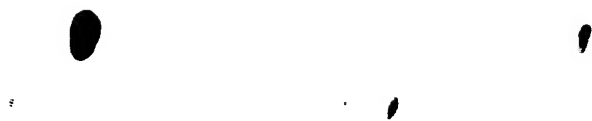


FIGURE 5

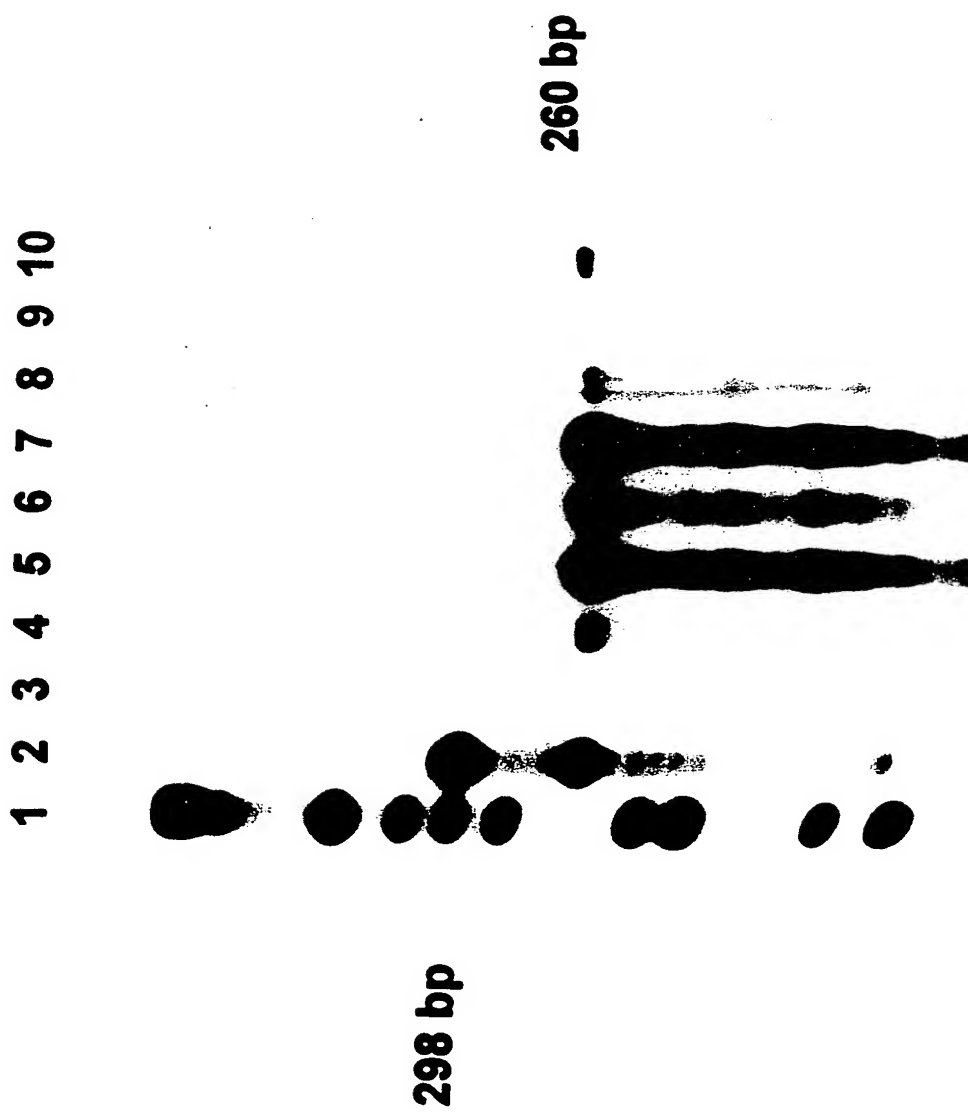


FIGURE 6

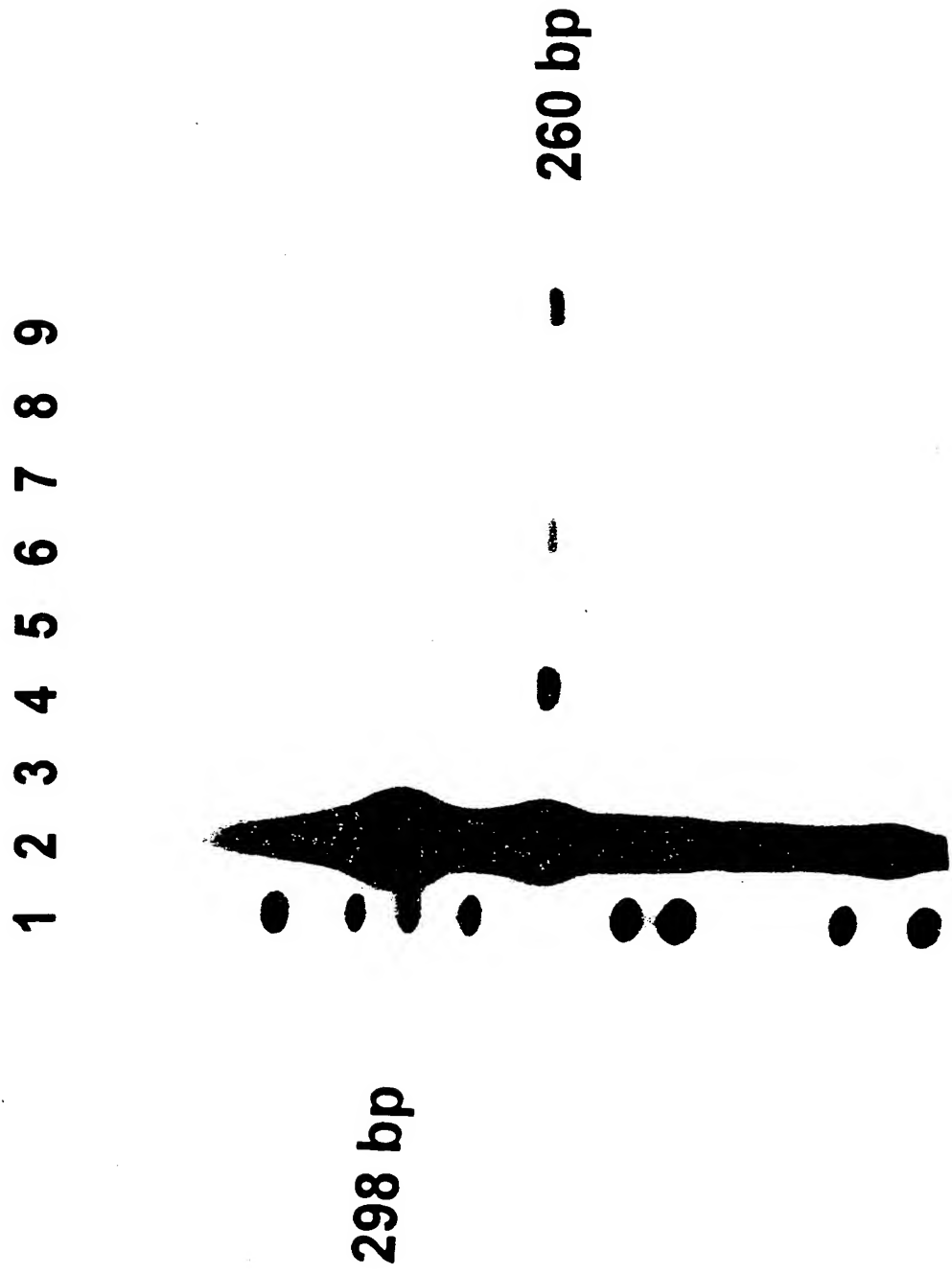


FIGURE 7

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

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FIGURE 8A

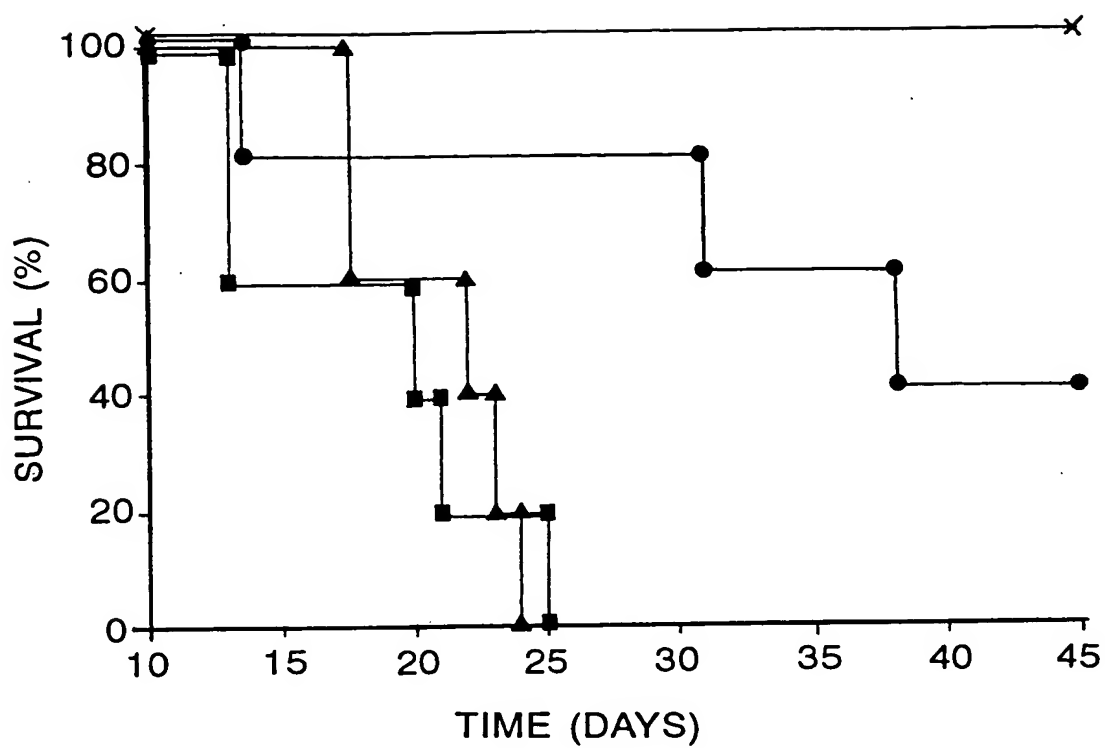


FIGURE 8B

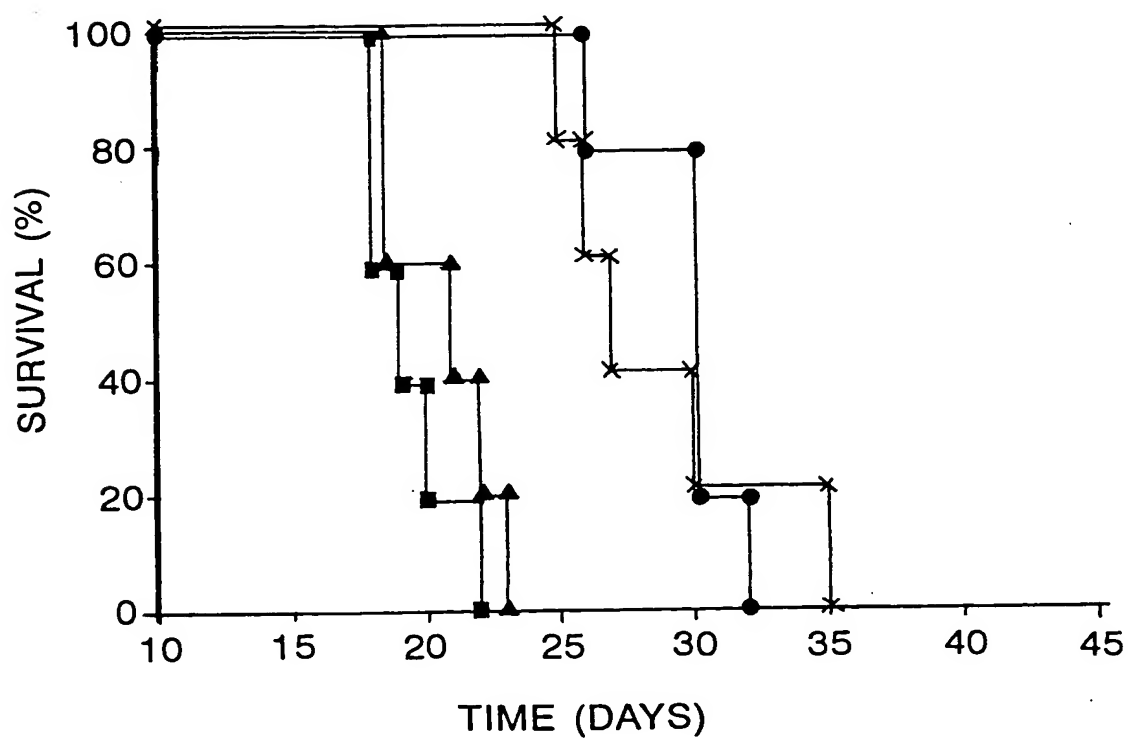


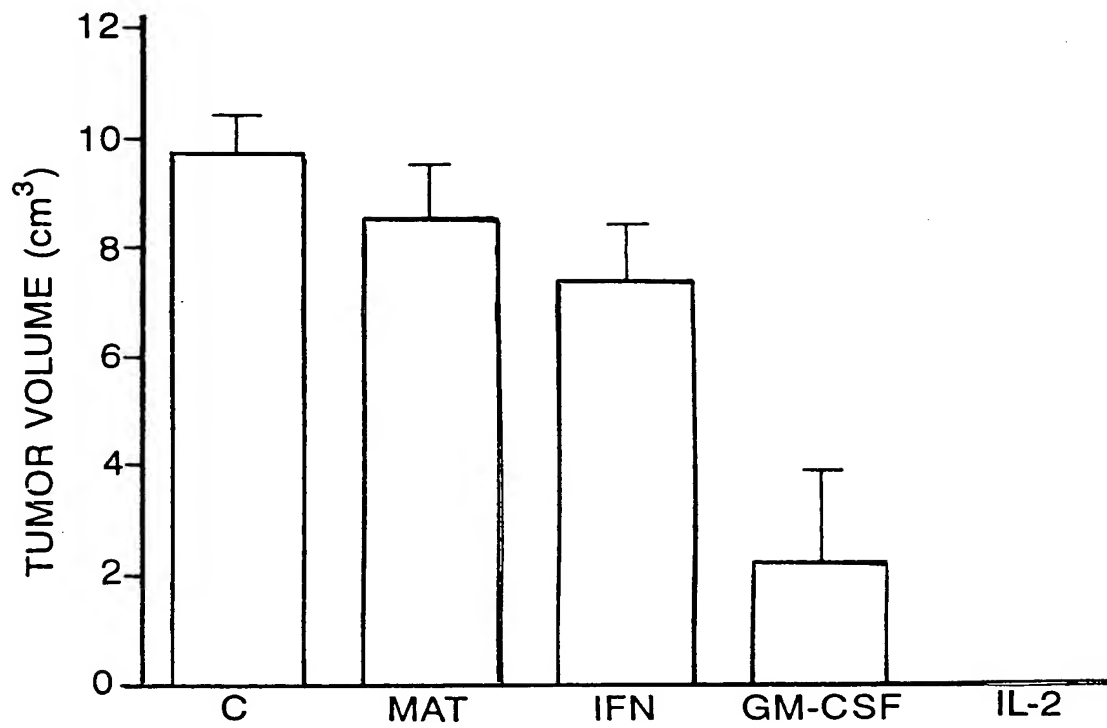
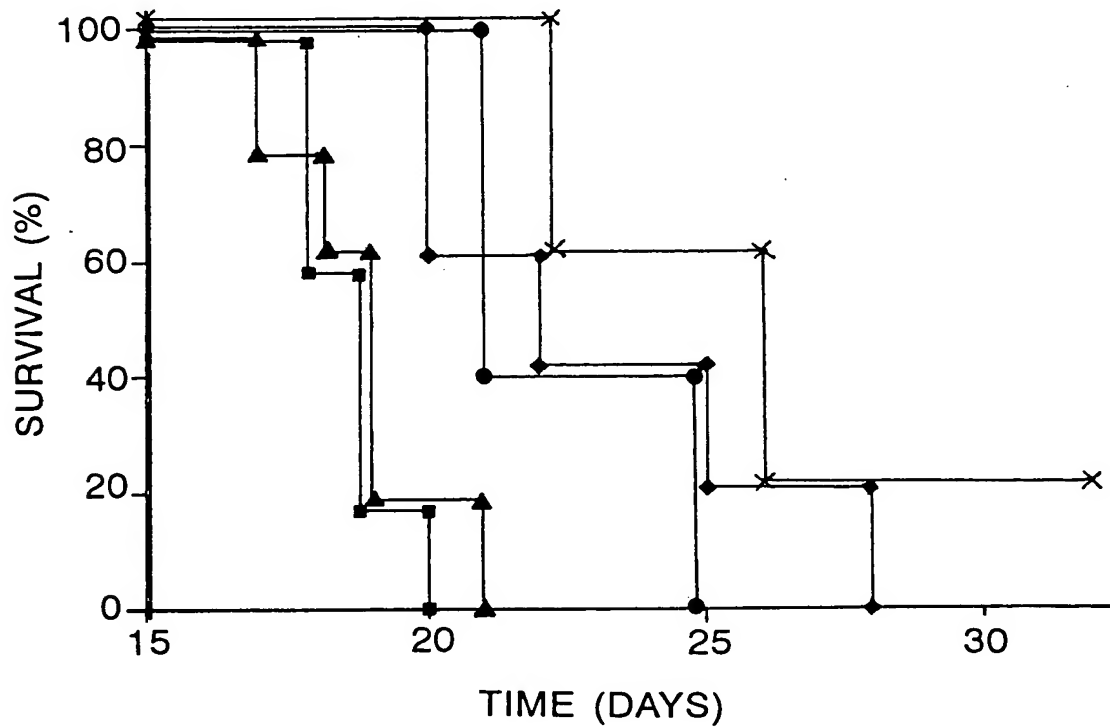
FIGURE 9A**FIGURE 9B**

FIGURE 10

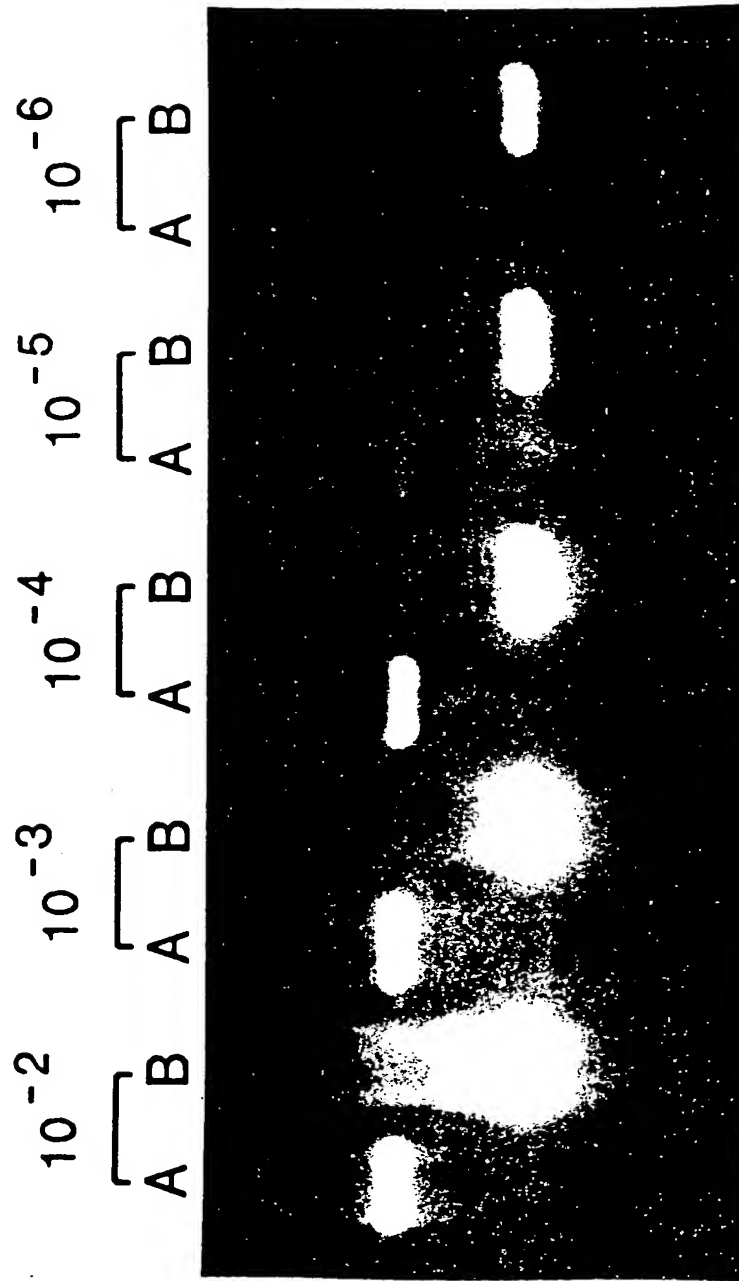


FIGURE 11

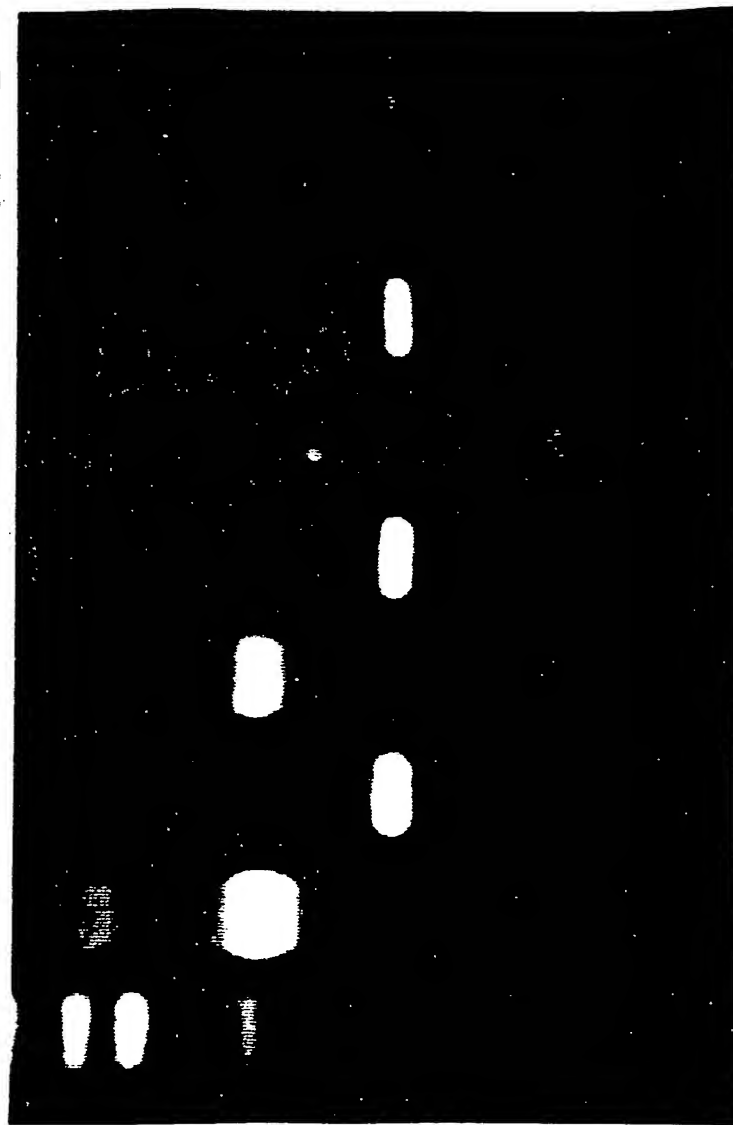
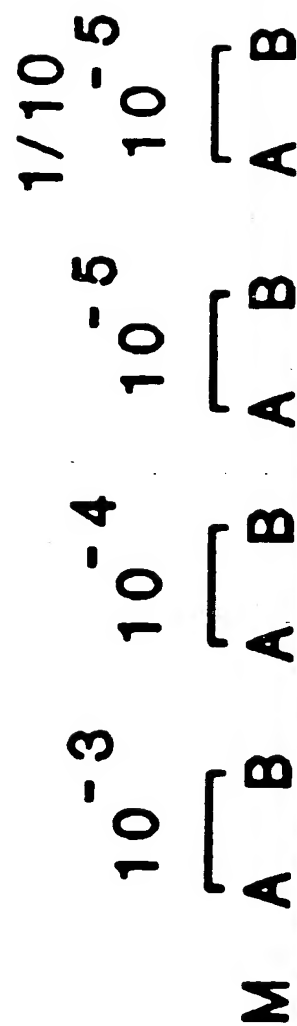


FIGURE 12

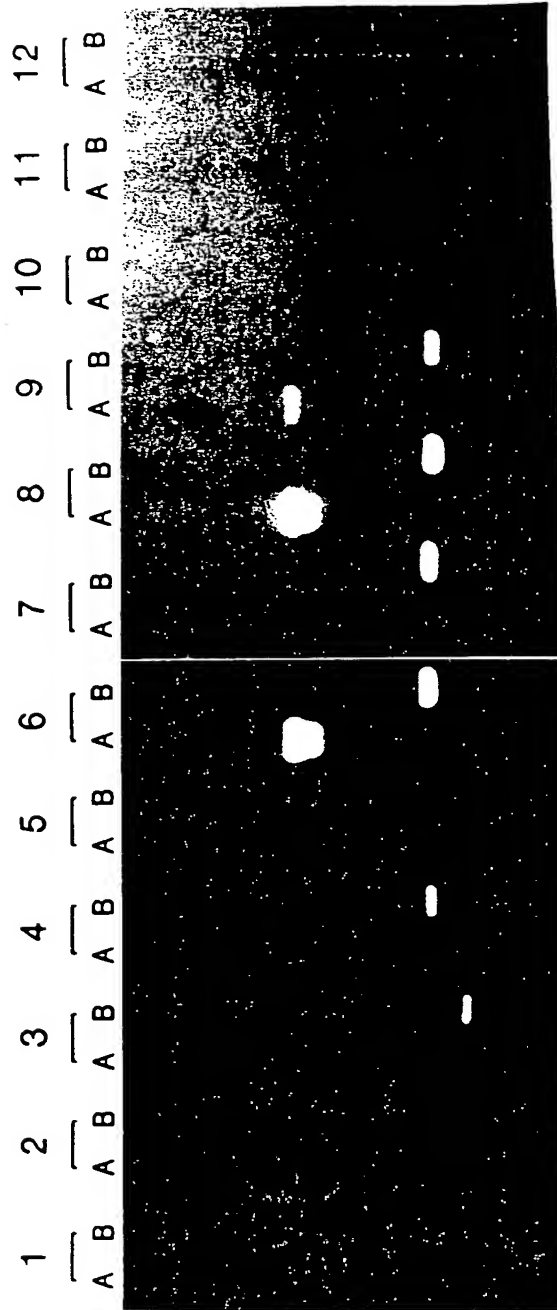


FIGURE 13

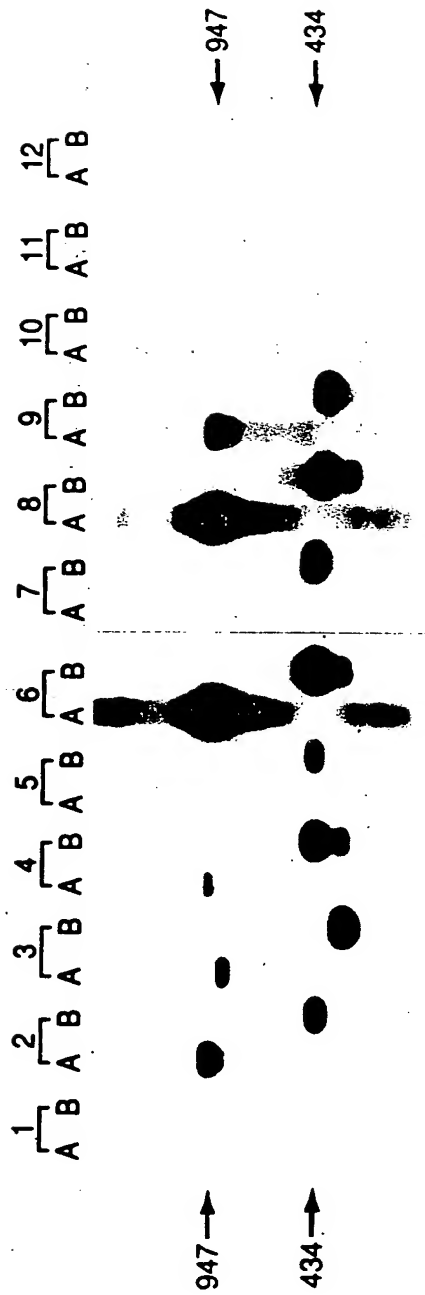


FIGURE 14

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	—	+
2	T2NoMo	RRP 7/93	6.1	—	—	+
3	T2CNoMo	PLND 5/93	4.5	0.1	—	+
4	T2BNoMo	RRP 3/92	NMA	0.4	—	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	—	+
6	Recur T3	I-125 1986	54.7	1.4	—	+
7	T3ANoMo	RRP 10/92	NMA	0.3	—	+
8	T3NxMo	XRT 1987	7.5	0.1	—	—
9	T3NxMo	Proscar + Flutamide	35.4	0.7	—	—
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	—	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	—	—
14	D1	PLND 1989 XRT 1989	1.6	0.4	—	—
15	D1	Proscar + Flutamide	20.8	0.5	—	—
16	T2CNoMo	RRP 4/92	0.1	0.3	—	—

FIGURE 15A

	10	20	30	40	50	60
1	GCGCCTTAAA	AAAAAAAAAAC	TTTCTTGGA	AATGTCCAGC	TCTTGCTTAA	ATATAAAAAT
	CGCGGAATTT	TTTTTTTTTG	AAAGAACCTT	TTACAGGTCG	AGAACGAATT	TATATTTTTTA
61	GAAAGGAAGA	AAGAGACTCT	CCTCTCTCCA	CTCCTATAAT	TATGAGGAAC	TTTTATTCAA
	CTTTCCTTCT	TTCTCTGAGA	GGAGAGAGGT	GAGGATATTA	ATACTCCTTG	AAAATAAGTT
121	CTCTGAAATT	CTATACAATC	TCTACAATAC	TCTACTGAAT	AAAAGCAGAG	CAGAAAAAGC
	GAGACTTTAA	GATATGTTAG	AGATGTTATG	AGATGACTTA	TTTTCGTCTC	GTCTTTTTCG
181	TGCGCTTTTT	TTCCATAGTC	GGGAATGCTT	GTCATCAGTG	TAAATCACCA	CCGCGCCCTT
	ACGCGAAAAA	AAGGTATCAG	CCCTTACGAA	CAGTAGTCAC	ATTTAGTGGT	GGCGCGGGAA
241	TTTCCTAAAG	AATATTATTG	TTATTAATAA	ACATGTAGGG	TATTATCCTC	CACTTACATT
	AAAGGATTTT	TTATAATAAC	AATAATTATT	TGTACATCCC	ATAATAGGAG	GTGAATGTAA
301	ACAAAACCAT	TTTTTAAAGC	CGGGCGTGGT	GGCTCACGCC	TGTAATCCCA	GCACTTTGGG
	TGTTTTGGTA	AAAAATTTTG	GCCCGCACCA	CCGAGTGC GG	ACATTAGGGT	CGTGAAACCC
361	AGGCCCAGAC	AGGCGGATCA	CGAAGTCGAG	AAATCGAGAC	CATCCTGGCC	AACATGGTGA
	TCCGGGTCTG	TCCGCCTAGT	GCTTCAGCTC	TTTAGCTCTG	GTAGGACCGG	TTGTACCACT
421	AACCCCATCT	CTACTAAAAA	TACAAAAATT	AGCTGGGCGT	GGTGGCGGGC	TCCTGTAGTC
	TTGGGGTAGA	GATGATTTTT	ATGTTTTTTA	TCGACCCGCA	CCACCGCCCG	AGGACATCAG
481	CCAGCTACTC	AGGAGGCTGA	GGCAGGAGAA	TCGCTTGAAC	CGGGGAGGCG	GAGGTTGCAG
	GGTCGATGAG	TCCTCCGACT	CCGTCCTCTT	AGCGAACTTG	GCCCCCTCCG	CTCCAACGTC
541	TCAGCCAAGA	TAGCGCCACT	GCACTGGAGC	CTGGTGACAG	AGTGAGACTC	CCTCAAGAAA
	AGTCGGTTCT	ATCGCGGTGA	CGTGACCTCG	GACCACTGTC	TCACTCTGAG	GGAGTTCTTT
601	GAAAGGAAGG	GAAGGGAAAG	GGAAGGAAGG	GGAGGGGAAG	GGAGGGGAGG	GGAGGGGAGG
	CTTTCCTTCC	CTTCCCTTTC	CCTTCCTTCC	CCTCCCTTTC	CCTCCCTTCC	CCTCCCTTCC
661	AAAGAAAAGA	ATACTGGAAC	TTGTTGAAGG	CAGAGACTTT	ATTTTCATAT	CCCGGCTATG
	TTTCTTTTCT	TATGACCTTG	AACAACCTCC	GTCTCTGAAA	TAAAAGTATA	GGGCCGATAC
721	TCTGGCTACT	GTCTTACGTA	ATAGATATAA	AATCAATCTT	GGTTGGATTA	ACCAGAAGAA
	AGACCGATGA	CAGAATGCAT	TATCTATATT	TTAGTTAGAA	CCAACCTAAT	TGGTCTTCTT

FIGURE 15B

781 TGAGAAGATA TATTCTGGTA AGTTGAATAC TTAGCACCCA GGGGTAATCA GCTTGGACAG
 ACTCTTCTAT ATAAGACCAT TCAACTTATG AATCGTGGGT CCCCATTAGT CGAACCTGTC

841 GACCAGGTCC AAAGACTGTT AAGAGTCTTC TGA CTCAAAA CTCAGTGCTC CCTCCAGTGC
 CTGGTCCAGG TTTCTGACAA TTCTCAGAAG ACTGAGGTTT GAGTCACGAG GGAGGTCACG

901 CACAAGCAAA CTCCATAAAG GTATCCTGTG CTGAATAGAG ACTGTAGAGT GGTACAAAGT
 GTGTTGTTT GAGGTATTTC CATAGGACAC GACTTATCTC TGACATCTCA CCATGTTTCA

961 AAGACAGACA TTATATTAAG TCTTAGCTTT GTGACTTCGA ATGACTTACC TAATCTAGCT
 TTCTGTCTGT AATATAATTC AGAATCGAAA CACTGAAGCT TACTGAATGG ATTAGATCGA

1021 AAATTTTCAGT TTTACCATGT GTAAATCAGG AAGAGTAATA GAACAAACCT TGAAGGGTCC
 TTTAAAGTCA AAATGGTACA CATTTAGTCC TTCTCATTA CTTGTTTGGG ACTTCCCAGG

1081 CAATGGTGAT TAAATGAGGT GATGTACATA ACATGCATCA CTCATAATAA GTGCTCTTTA
 GTTACCACTA ATTTACTCCA CTACATGTAT TGTACGTAGT GAGTATTATT CACGAGAAAT

1141 AATATTAGTC ACTATTATTA GCCATCTCTG ATTAGATTG ACAATAGGAA CATTAGGAAA
 TTATAATCAG TGATAATAAT CGGTAGAGAC TAATCTAAAC TGTTATCCTT GTAATCCTTT

1201 GATATAGTAC ATTCAGGATT TTGTTAGAAA GAGATGAAGA AATTCCCTTC CTTCCTGCCC
 CTATATCATG TAAGTCCTAA AACAATCTTT CTCTACTTCT TTAAGGGAAG GAAGGACGGG

1261 TAGGTCATCT AGGAGTTGTC ATGGTTTCATT GTTGACAAAT TAATTTTCCC AAATTTTTC
 ATCCAGTAGA TCCTCAACAG TACCAAGTAA CAACTGTTTA ATTAAAAGGG TTTAAAAAGT

1321 CTTTGCTCAG AAAGTCTACA TCGAAGCACC CAAGACTGTA CAATCTAGTC CATCTTTTTC
 GAAACGAGTC TTTGAGATGT AGCTTCGTGG GTTCTGACAT GTTAGATCAG GTAGAAAAAG

1381 CACTTAACTC ATACTGTGCT CTCCCTTTCT CAAAGCAAAC TGTTTGCTAT TCCTTGAATA
 GTGAATTGAG TATGACACGA GAGGGAAAGA GTTTCGTTTG ACAAACGATA AGGAACCTAT

1441 CACTCTGAGT TTTCTGCCTT TGCCTACTCA GCTGGCCCAT GGCCCTAAT GTTCTTCTC
 GTGAGACTCA AAAGACGGAA ACGGATGAGT CGACCGGGTA CCGGGGATTA CAAAGAAGAG

1501 ATCTCCACTG GGTCAAATCC TACCTGTACC TTATGGTTCT GTTAAAAGCA GTGCTTCCAT
 TAGAGGTGAC CCAGTTTAGG ATGGACATGG AATACCAAGA CAATTTTCGT CACGAAGGTA

1561 AAAGTACTCC TAGCAAATGC ACGGCCTCTC TCACGGATTA TAAGAACACA GTTTATTTTA
 TTTGATGAGG ATCGTTTACG TGCCGGAGAG AGTGCCTAAT ATTCTTGTGT CAAATAAAAT

1621 TAAAGCATGT AGCTATTCTC TCCCTCGAAA TACGATTATT ATTATTAAGA ATTTATAGCA
 ATTTTCGTACA TCGATAAGAG AGGGAGCTTT ATGCTAATAA TAATAATTCT TAAATATCGT

1681 GGGATATAAT TTTGTATGAT GATTCTTCTG GTTAATCCAA CCAAGATTGA TTTTATATCT
 CCTATATTA AAACATACTA CTAAGAAGAC CAATTAGGTT GTTCTAACT AAAATATAGA

1741 ATTACGTAAG ACAGTAGCCA GACATAGCCG GGATATGAAA ATAAAGTCTC TGCCTTCAAC
 TAATGCATTC TGTGATCGGT CTGTATCGGC CCTATACCTT TATTTGAGAG ACGGAAGTTG

1801 AAGTTCCAGT ATTCTTTTCT TTCTCTCCCT CCCCTCCCT CCCTTCCCT CCCCTTCCCT
 TTCAAGGTCA TAAGAAAAGA AAGGAGGGGA GGGGAGGGGA GGGGAGGGGA GGGGAAGGAA

1861 CCCTTTCCCT TCCCTTCCTT TCTTTCTTGA GGGAGTCTCA CTCTGTCACC AGGCTCCAGT
 GGGAAAGGGA AGGGAAGGAA AGAAAGAACT CCTCAGAGT GACACAGTGG TCCGAGGTCA

FIGURE 15C

1921 GCAGTGGCGC TATCTTGGCT GACTGCAACC TCCGCTCCC CGGTTCAAGC GATTCTCCTG
 CGTCACCGCG ATAGAAACCGA CTGACGTTGG AGGCGGAGGG GCCAAGTTCC CTAAGAGGAC

1981 CCTCAGCCTC CTGAGTAGCT GGGACTACAG GAGCCCGCCA CCACGCCAG CTAATTTTGG
 GGAGTCGGAG GACTCATCGA CCCTGATGTC CTCGGGCGGT GGTGCGGGTC GATTAAAAAC

2041 TATTTTGTAGT AGAGATGGGG TTTCAACATG TTGGCCAGGA TGGTCTCGAT TTCTCGACTT
 ATAAAAATCA TCTCTACCCC AAAGTGGTAC AACCGGTCCT ACCAGAGCTA AAGAGCTGAA

2101 CGTGATCCGC CTGTCTGGGC CTCCCAAAGT GCTGGGATTA CAGGCGTGAG CCACCACGCC
 GCACTAGGCG GACAGACCCG GAGGGTTTCA CGACCCTAAT GTCCGCACTC GGTGGTGGCG

2161 CGGCTTTAAA AAATGGTTTT GTAATGTAAG TGGAGGATAA TACCCTACAT GTTTATTAAAT
 GCGAAATTT TTTACCAAAA CATTACATTC ACCTCCTATT ATGGGATGTA CAAATAATTA

2221 AACAAATAATA TTCTTTAGGA AAAAGGGGCG GGTGGTGATT TACACTGATG ACAAGCATTG
 TTGTTATTAT AAGAAATCCT TTTTCCCGCG CCACCACTAA ATGTGACTAC TGTTGCTAAG

2281 CCGACTATGG AAAAAAAGCG CAGCTTTTTT TGCTCTGCTT TTATTCAGTA GAGTATTGTA
 GGCTGATACC TTTTTTTCGC GTCGAAAAAG ACGAGACGAA AATAAGTCAT CTCATAACAT

2341 GAGATTGTAT AGAATTTTCAG AGTTGAATAA AAGTTCCTCA TAATTATAGG AGTGGAGAGA
 CTCTAACATA TCTTAAAGTC TCAACTTATT TTCAAGGAGT ATTAATATCC TCACCTCTCT

2401 GGAGAGTCTC TTTCTTCCTT TCATTTTTAT ATTTAAGCAA GAGCTGGACA TTTTCCAAGA
 CCTCTCAGAG AAAGAAGGAA AGTAAAAATA TAAATTCGTT CTCGACCTGT AAAAGGTTCT

2461 AAGTTTTTTT TTTTAAAGGC GCCTCTCAAA AGGGGCGGGA TTTCTTCTC CTGGAGGCAG
 TTCAAAAAAA AAAAATTCGG CGGAGAGTTT TCCCCGGCCT AAAGGAAGAG GACCTCCGTC

2521 ATGTTGCCCTC TCTCTCTCGC TCGGATTGGT TCAGTGCCTC CTAGAAACAC TGCTGTGGTG
 TACAACGGAG AGAGAGAGCG AGCCTAACCA AGTCACGTGA GATCTTTGTG ACGACACCAC

2581 GAGAACTGG ACCCCAGGTC TGGAGCGAAT TCCAGCCTGC AGGGCTGATA AGCGAGGCAT
 CTCTTTGACC TGGGGTCCAG ACCTCGCTTA AGGTGGGAGC TCCCGACTAT TCGCTCCGTA

2641 TAGTGAGATT GAGAGAGACT TTACCCCGCC GTGGTGTTG GAGGGCGCGC AGTAGAGCAG
 ATCACTCTAA CTCTCTCTGA AATGGGGCGG CACCACCAAC CTCCCGCGCG TCATCTCCTC

2701 CAGCACAGGC CGGGGTCCCG GGAGGCCGGC TCTGCTCGCG CCGAGATGTG GAATCTCCTT
 GTCGTGTCCG CGCCCAAGGC CCTCCGGCCG AGACGAGCCG GGCTCTACAC CTTAGAGGAA

2761 CACGAAACCG ACTCGGCTGT GCCACCGCG CGCCGCCCGC GCTGGCTGTG CGCTGGGGCG
 GTGCTTTGGC TGAGCGGACA CCGGTGGCGC GCGGCGGGCG CGACCGACAC GCGACCCCGC

2821 CTGGTGCTGG CGGGTGCTT CTTTCTCCTC GGCTTCCTCT TCGGTAGGGG GCGGCTCGC
 GACCACGACC GCCCACCGAA GAAAGAGGAG CCGAAGGAGA AGCCATCCCC CCGCGGAGCG

2881 GGAGCAAACC TCGGAGTCTT CCCCCTGGTG CCGCGGTGCT GGGACTCGCG GGTGAGCTGC
 CCTCGTTTGG AGCCTCAGAA GGGGCACCAC GGCGCCACGA CCCTGAGCGC CCACTCGAGC

2941 CGAGTGGGAT CCTGTTGCTG GTCTTCCCA GGGGCGGCGA TTAGGGTCGG GGTAAATGTGG
 GCTCACCCTA GGACAACGAC CAGAAGGGGT CCCCAGCGCT AATCCCAGCC CCATTACACC

3001 GGTGAGCACC CCTCGAG
 CCACTCGTGG GGAGCTC

FIGURE 15D

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- 2401 GGAGAGTCTC TTTCTTCCTT TCATTTTAT ATTTAAGCAA GAGCTGGACA TTTTCCAAGA
      CCTCTCAGAG AAAGAAGGAA AGTAAAAATA TAAATTCGTT CTCGACCTGT AAAAGGTTCT

- 2461 AAGT.TTTTTT TTTTAAAGGC GCCTCTCAAA AGGGGCCGGA TTTCCTTCTC CTGGAGGCAG
      TTCAAAAAAA AAAAATTCCG CGGAGAGTTT TCCCCGGCCT AAAGGAAGAG GACCTCCGTC

- 2521 ATGTTGCCTC TCTCTCTCGC TCGGATTGGT TCAGTGCAC TTAGAAACAC TGCTGTGGTG
      TACAACGGAG AGAGAGAGCG AGCCTAACCA AGTCACGTGA GATCTTTGTG ACGACACCAC

- 2581 GAGAAACTGG ACCCCAGGTC TGGAGCGAAT TCCAGCCTGC AGGGCTGATA AGCGAGGCAT
      CTCTTTGACC TGGGGTCCAG ACCTCGCTTA AGGTCCGACG TCCCGACTAT TCGCTCCGTA

- 2641 TAGTGAGATT GAGAGAGACT TTACCCCGCC GTGGTGGTTG GAGGGCGCGC AGTAGAGCAG
      ATCACTCTAA CTCTCTCTGA AATGGGGCGG CACCACCAAC CTCCCGCGCG TCATCTCGTC

- 2701 CAGCACAGGC GCGGGTCCCG GGAGGCCGGC TCTGCTCGCG CCGAGATGTG GAATCTCCTT
      GTCGTGTCCG CCCCCAGGGC CCTCCGGCCG AGACGAGCGG GGCTCTACAC CTTAGAGGAA

- 2761 CACGAAACCG ACTCGGCTGT GGCCACCGCG CGCCGCCCGC GCTGGCTGTG CGCTGGGGCG
      GTGCTTTGGC TGAGCCGACA CCGGTGGCGC GCGGCGGGCG CGACCGACAC GCGACCCCGC

- 2821 CTGGTGCTGG CGGGTGGCTT CTTTCTCCTC GGCTTCCTCT TCGGTAGGGG GGCGCCTCGC
      GACCACGACC GCCCACCGAA GAAAGAGGAG CCGAAGGAGA AGCCATCCCC CCGCGGAGCG

- 2881 GGAGCAAACC TCGGAGTCTT CCCCCTGGTG CCGCGGTGCT GGGACTCGCG GGTCAGCTGC
      CCTCGTTTGG AGCCTCAGAA GGGGCACCAC GGCGCCACGA CCCTGAGCGC CCAGTCGACG

- 2941 CGAGTGGGAT CCTGTTGCTG GTCTTCCCCA GGGGCGGCGA TTAGGGTCCG GGTAAATGTGG
      GTCACCCCTA GGACAACGAC CAGAAGGGGT CCCCGCCGCT AATCCCAGCC CCATTACACC

- 3001 GGTGAGCACC CCTCGAG
      CCACTCGTGG GGAGCTC

```

FIGURE 16**Potential binding sites on the PSM promoter***

Site	Seq	**Location	#nt matched
AP1	TKAGTCA	-1145	7/7
E2-RS	ACCNNNNNNGGT	-1940	12/12
		-1951	12/12
GHF	NNNTAAATNNN	-580	11/11
		-753	11/11
		-1340	11/11
		-1882	11/11
		-1930	11/11
		-1979	11/11
		-2001	11/11
		-2334	11/11
		-2374	11/11
		-2591	11/11
		-2620	11/11
		-2686	11/11
JVC repeat	GGGNGGRR	-1165	8/8
		-1175	8/8
		-1180	8/8
		-1185	8/8
		-1190	8/8
NFkB	GGGRHTYYHC	-961	10/10
uteroglobi	RYYWSGTG	-250	8/8
		-921	8/8
		-1104	8/8
IFN	AAWAANGAAAGGR	590	13/13
Cell 41:509 (1985)			

FIGURE 17

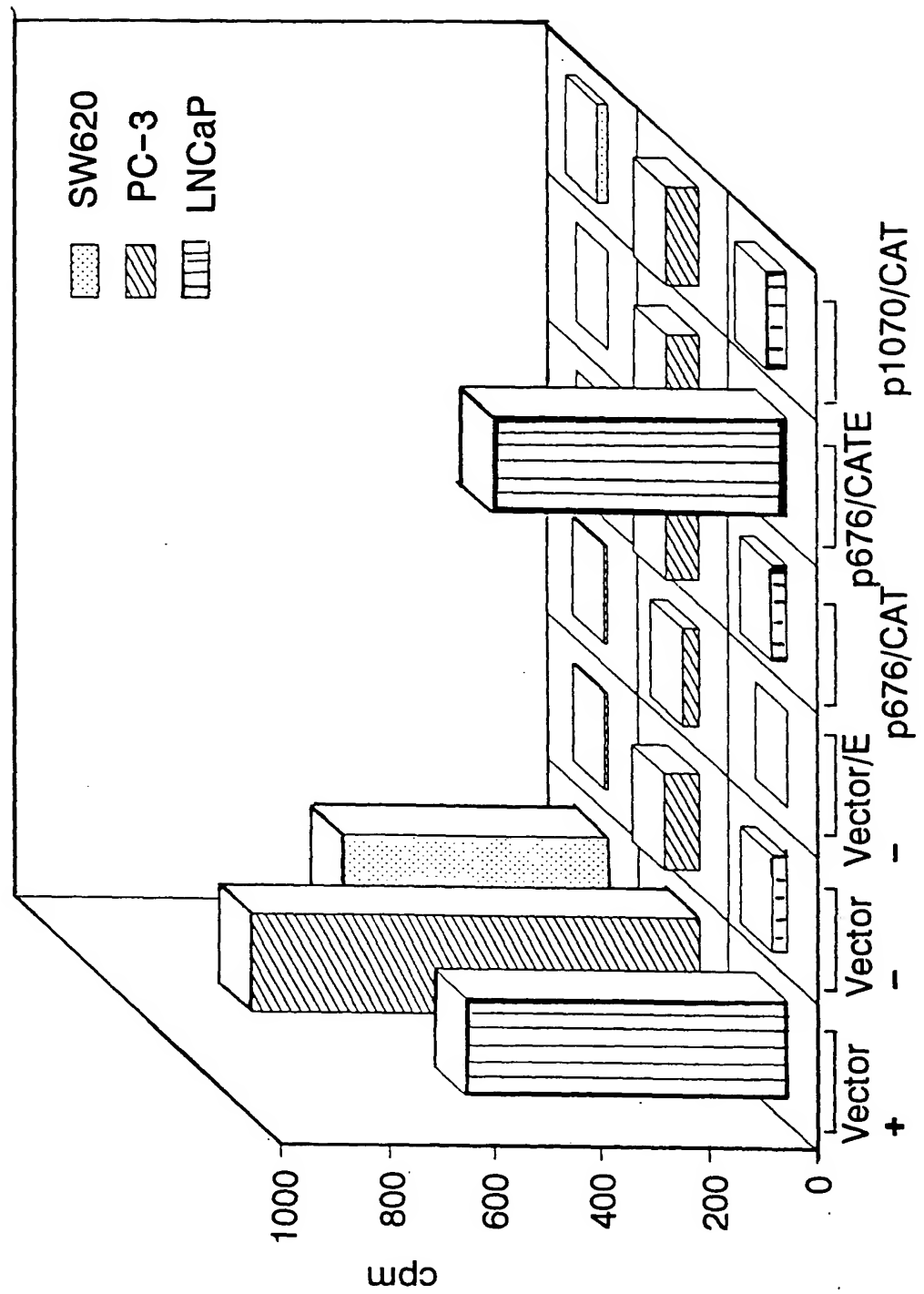


FIGURE 18

CTCAAAAGGGCCCGATTTTCCT

TCT TGGAGGCAGATGTGCCCTCTCTCTCTCGCTCGGATTGGTTTCAGTGCACCTCTAGAAACACTGCTGTGTGGAGAAACT
GGACCCC AGG TCTGGAGCGAATTCCA GCCTGCAGGGCTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCC
CGCGGTGGTGGAGGGCGGCAGT AGAGCAGCAGCACAGGCGCGGTCCCGGAGGCCGCTCTGCTCGGCCCGGAG

ATG TGG AAT CTC CTT CAC GAA ACC GAC TCG GCT GTG GCC ACC GCG CGC CGC CGC TGG CTG

Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Ala Arg Arg Pro Arg Trp Leu

TGC GCT GGG GCG CTG GTG CTG GCG GGT GGCTTC TTT CTC CTC GGC TTC CTC TTC GGA TGG TTT

Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe

ATA AAA TCC TCC AAT GAA GCT ACT AAC ATT ACT CCA AAG CAT AAT ATG AAA GCA TTT TTG GAT GAA
Ile Lys Ser Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
*

TGG AAA GCT GAG AAC ATC AAG AAG TTC TTA TAT AAT TTT ACA CAG ATA CCA CAT TTA GCA GGA ACA
Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr

FIGURE 19

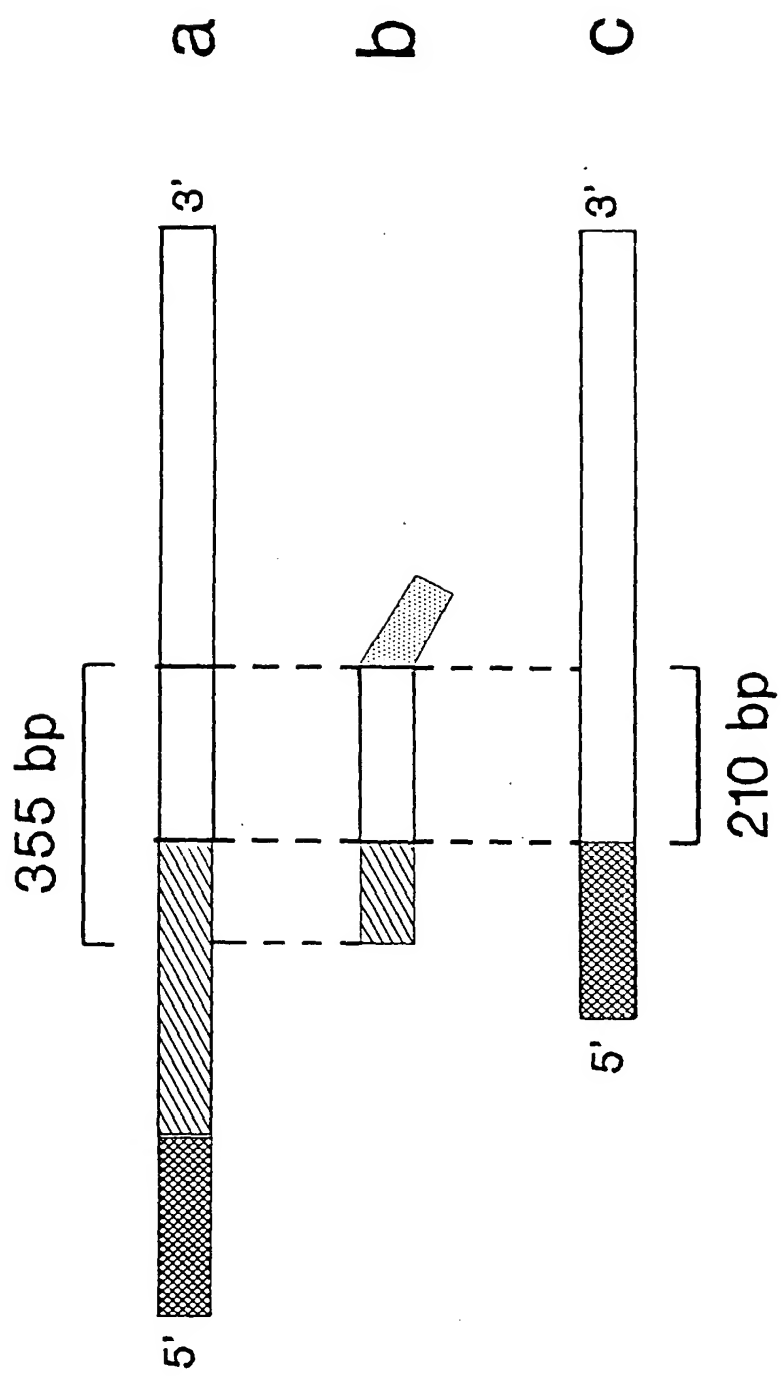
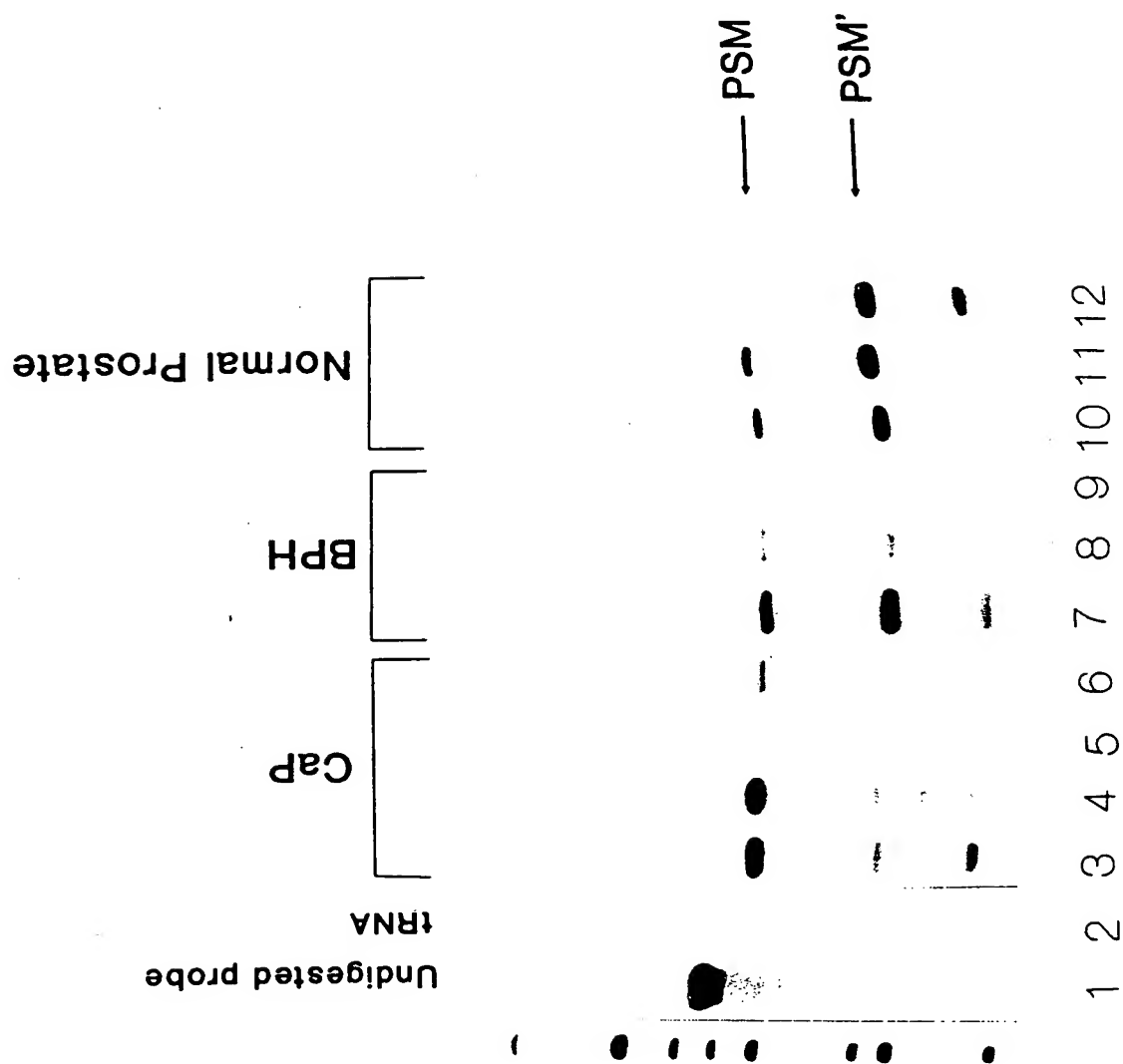
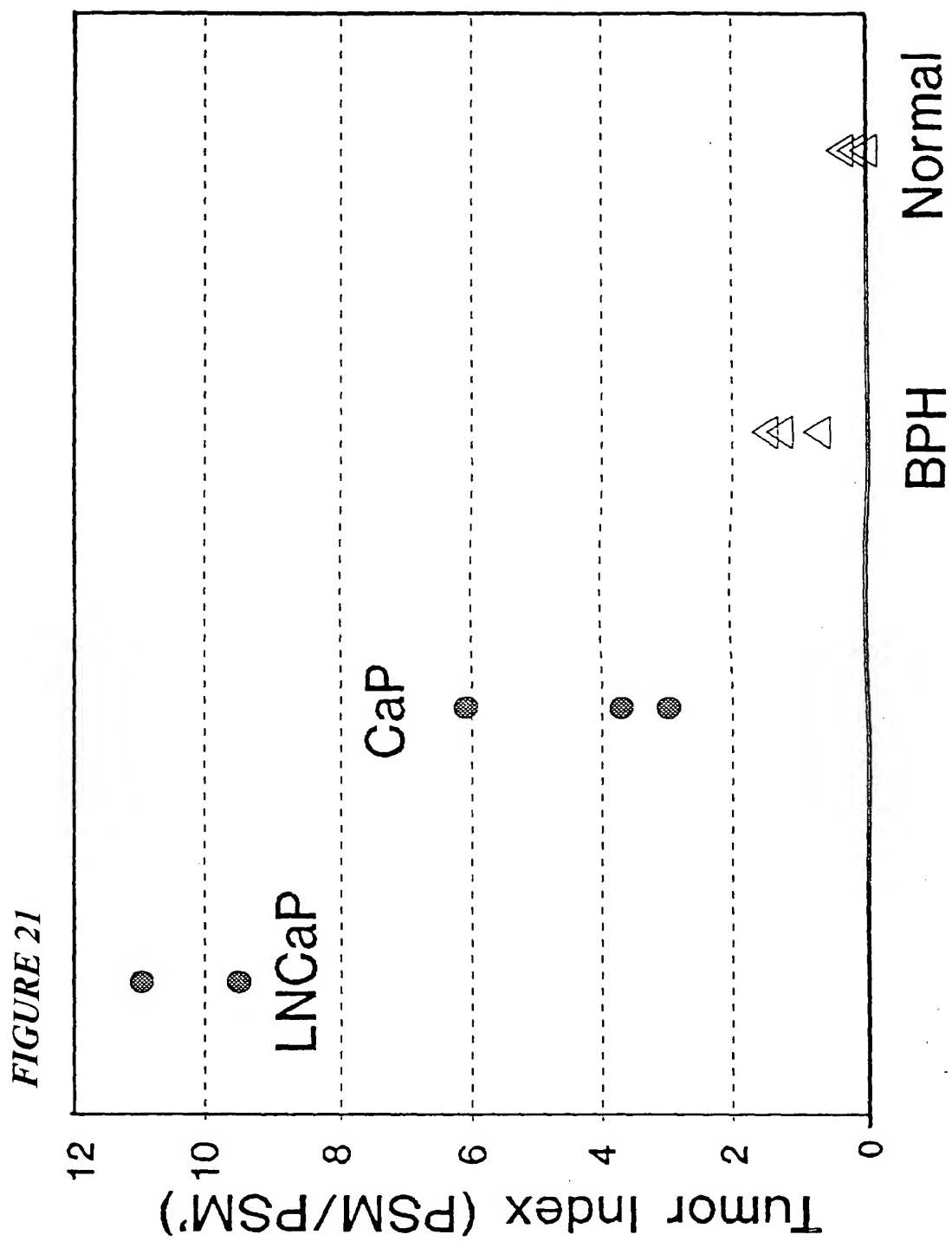


FIGURE 20





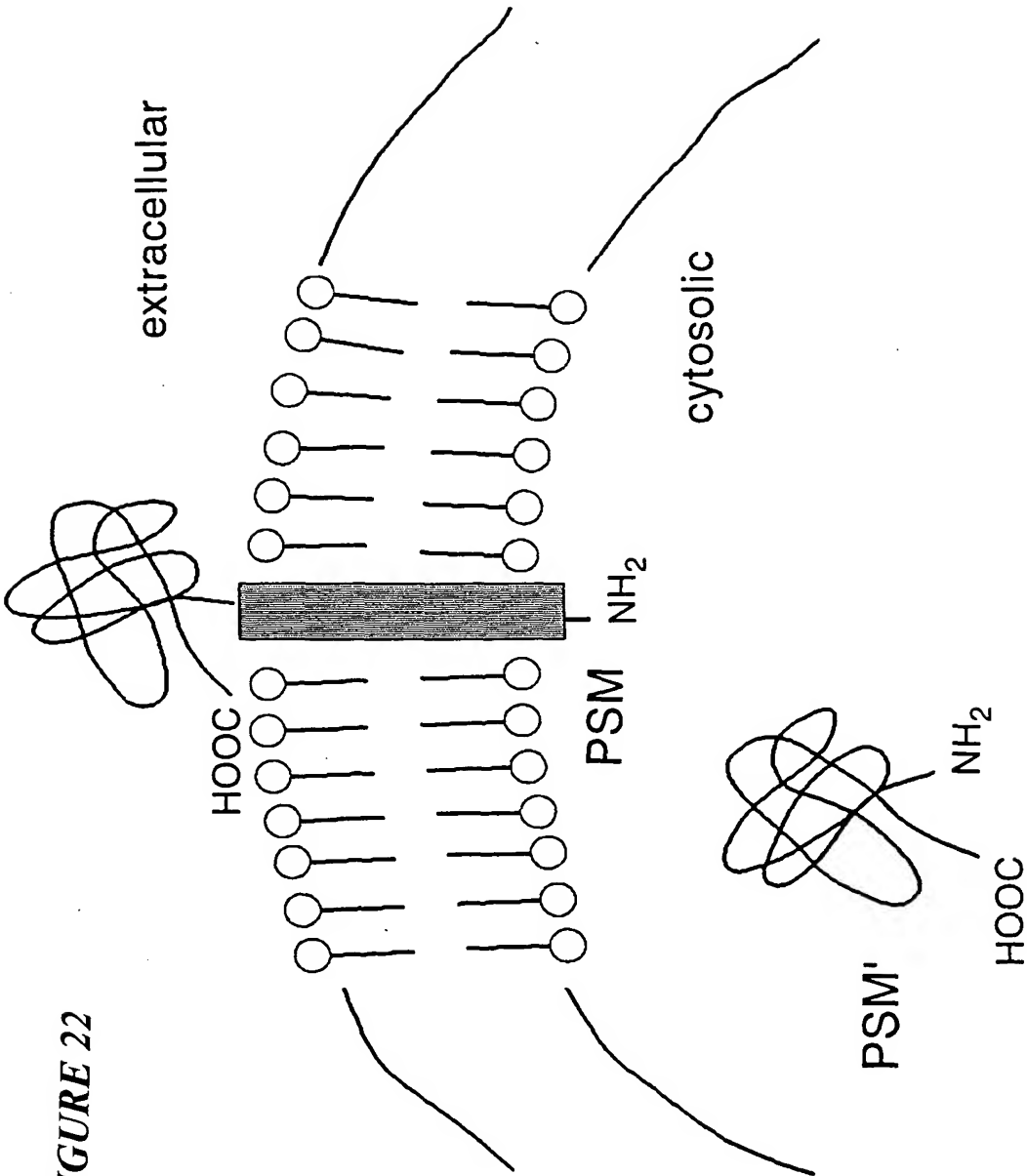


FIGURE 22

FIGURE 23

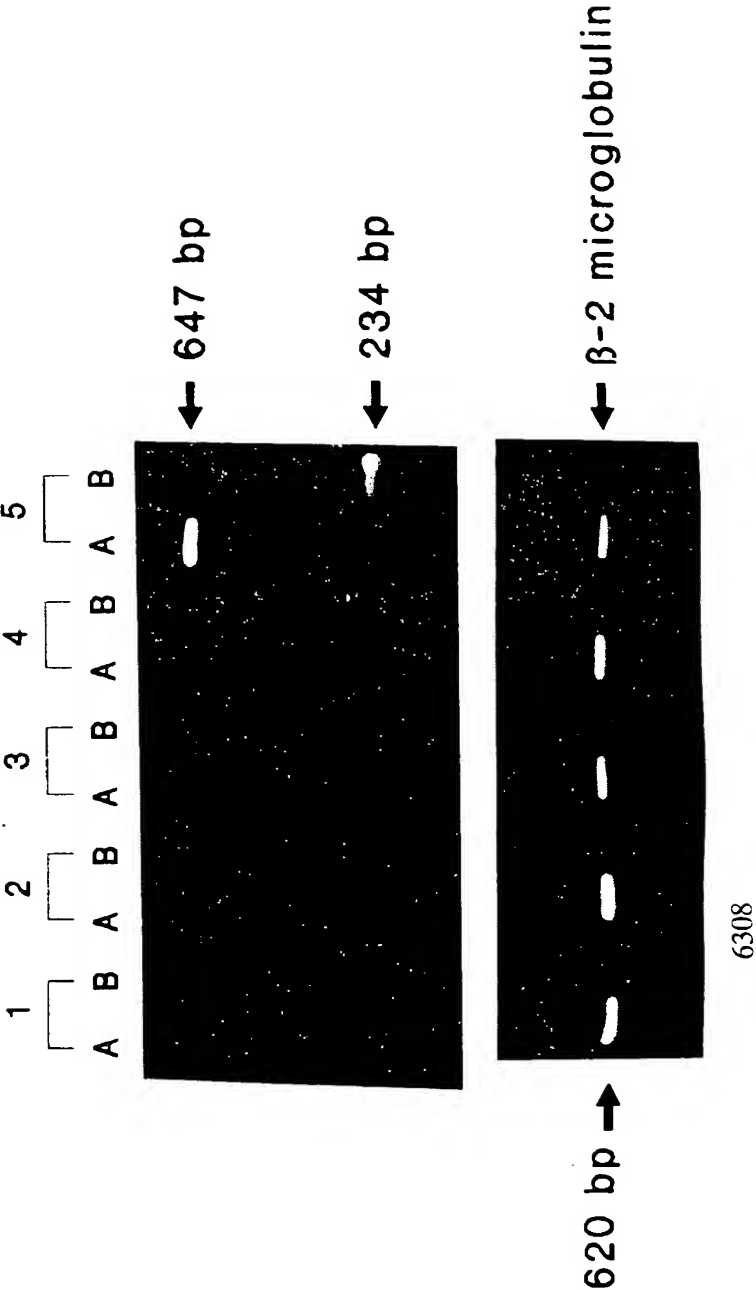
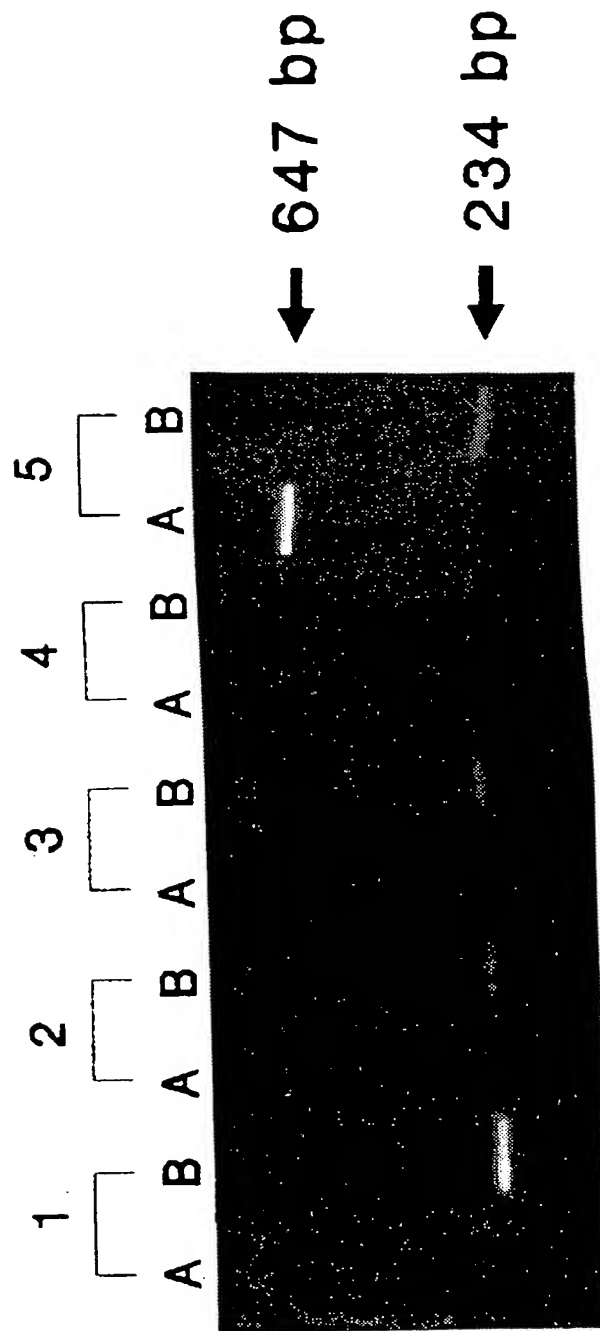


FIGURE 24



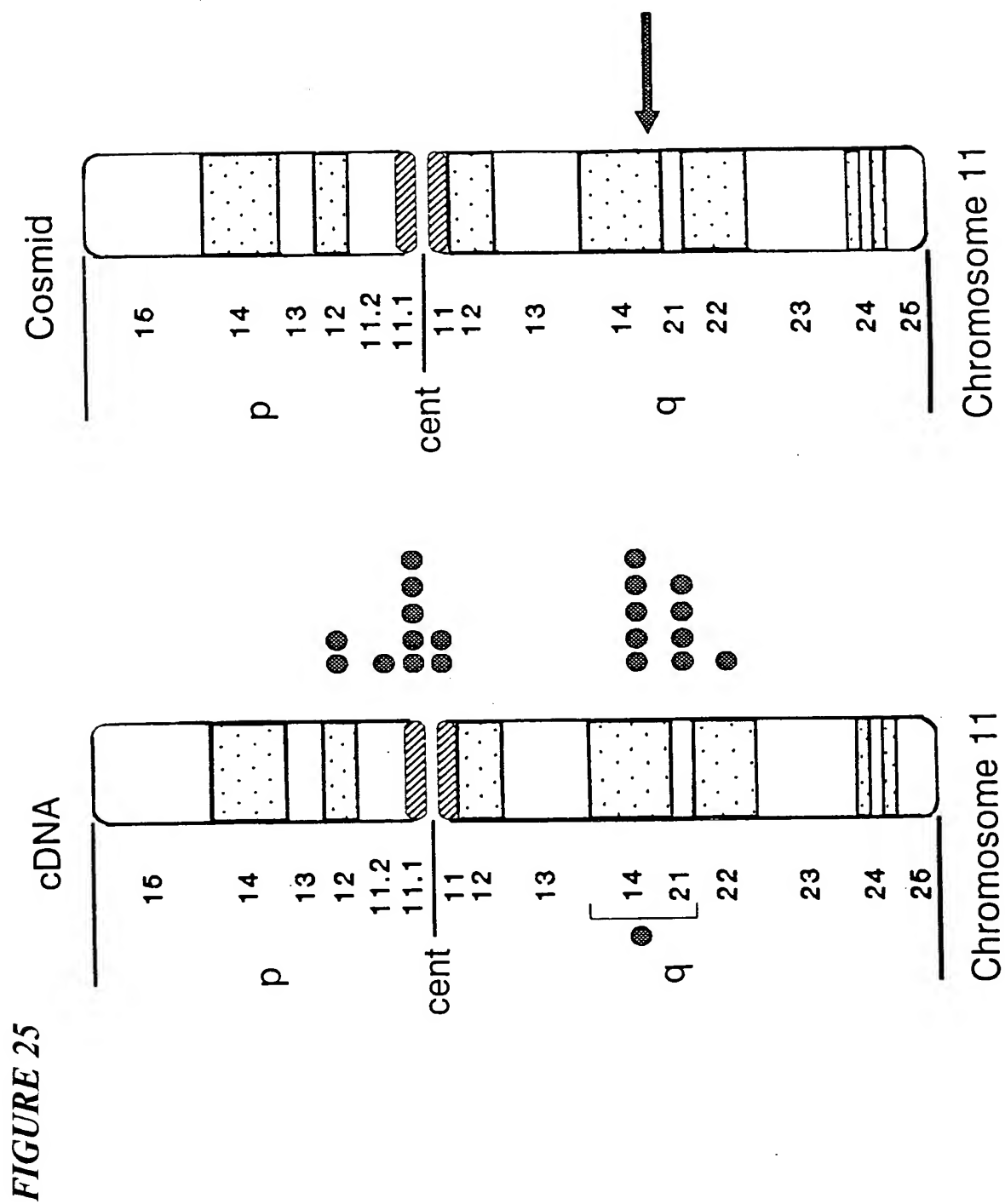


FIGURE 26

♂ ♀ M H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

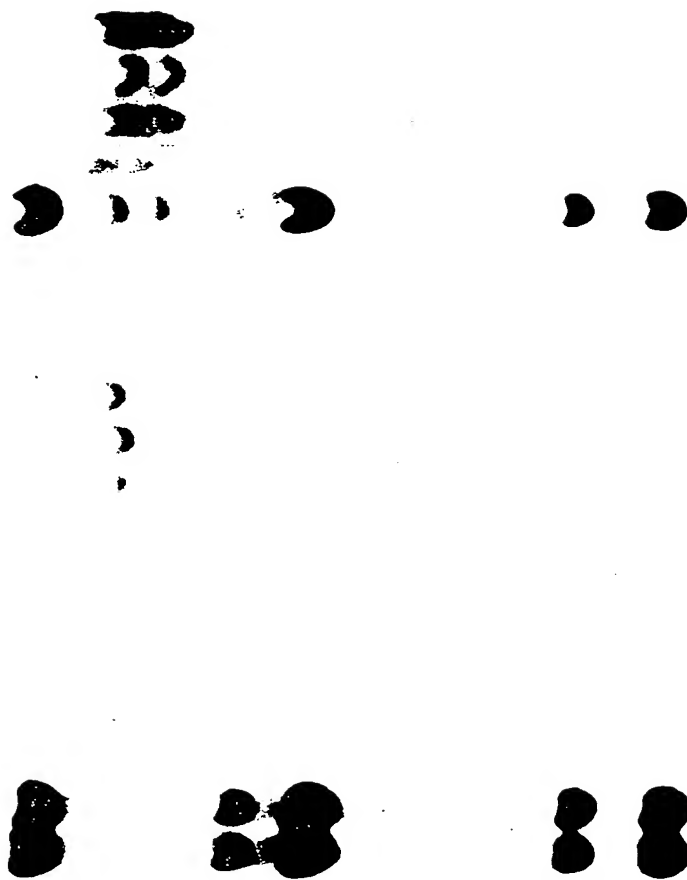


FIGURE 27

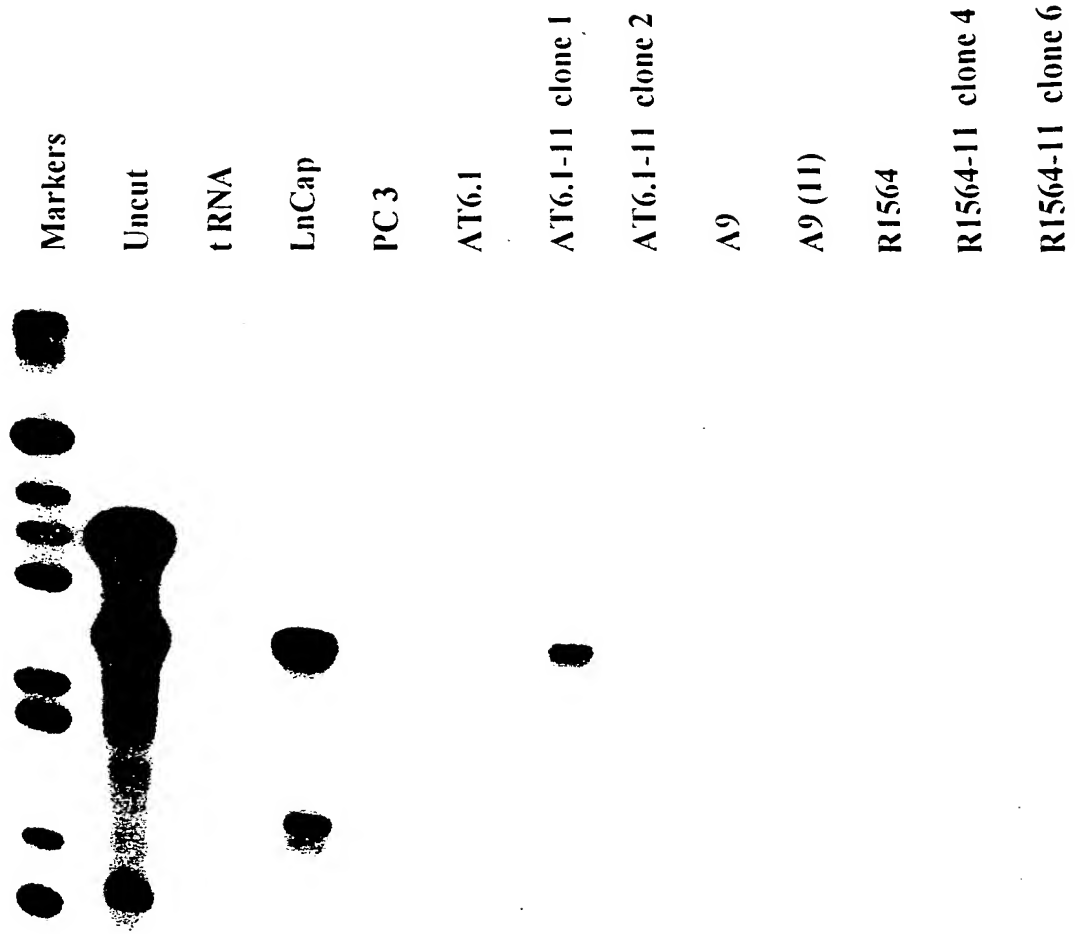


FIGURE 28

TISSUE/ CELL LINE	CANCER CELL TYPE	¹ PSM DNA	² PSM RNA
HUMAN PROSTATE	N.A.	+	+
HUMAN MAMMARY	N.A.	+	-
AT6.1	RAT PROSTATIC ADENOCARCINOMA	-	-
AT6.1-11-CL1	"	+	+
AT6.1-11-CL2	"	-	-
R1564	RAT MAMMARY ADENOCARCINOMA	-	-
R1564-11-CL2	"	+	-
R1564-11-CL4	"	+	-
R1564-11-CL5	"	+	-
R1564-11-CL6	"	+	-
A9	MOUSE FIBROSARCOMA	-	-
A9(11)	"	+	-

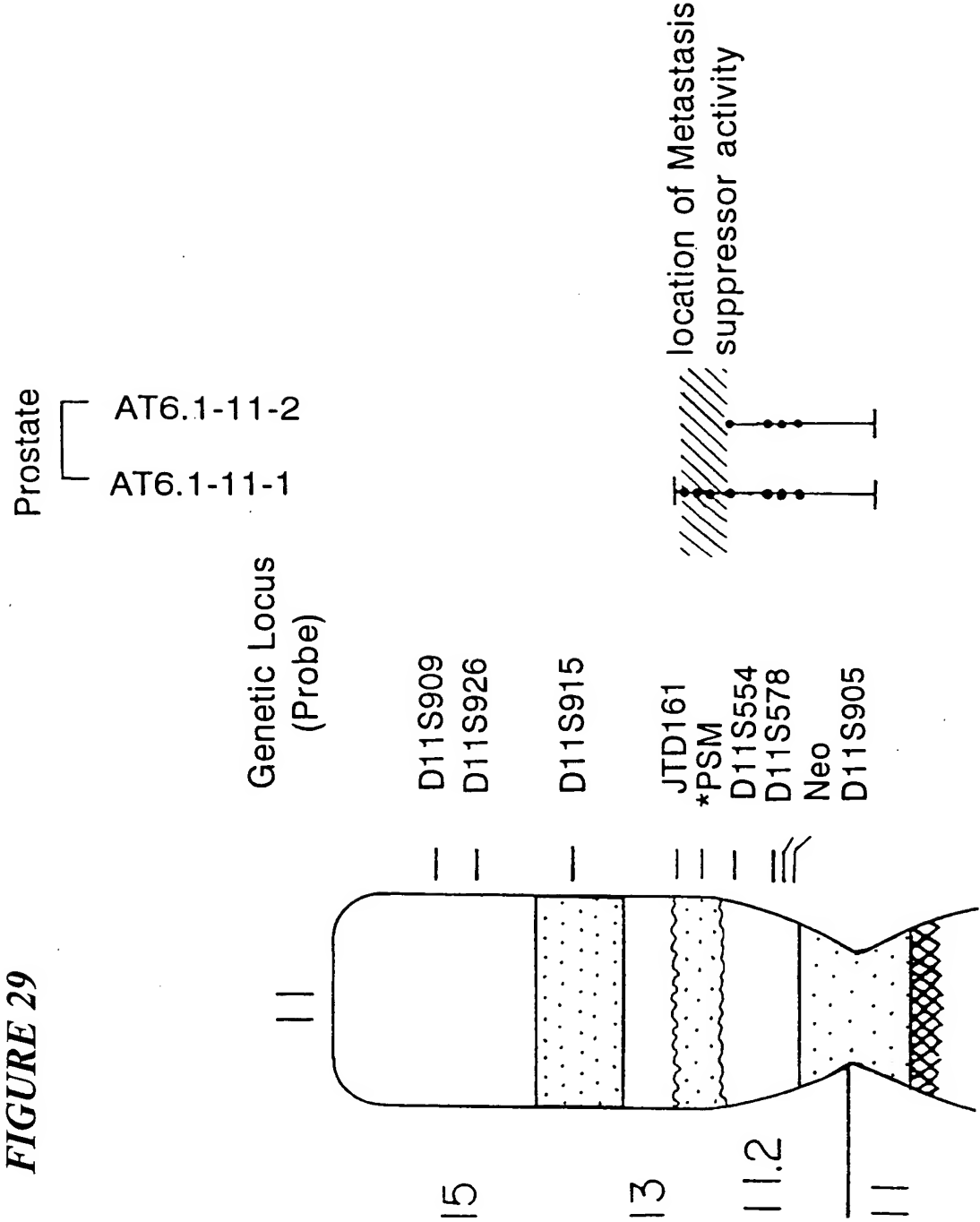


FIGURE 30

FIG. 55

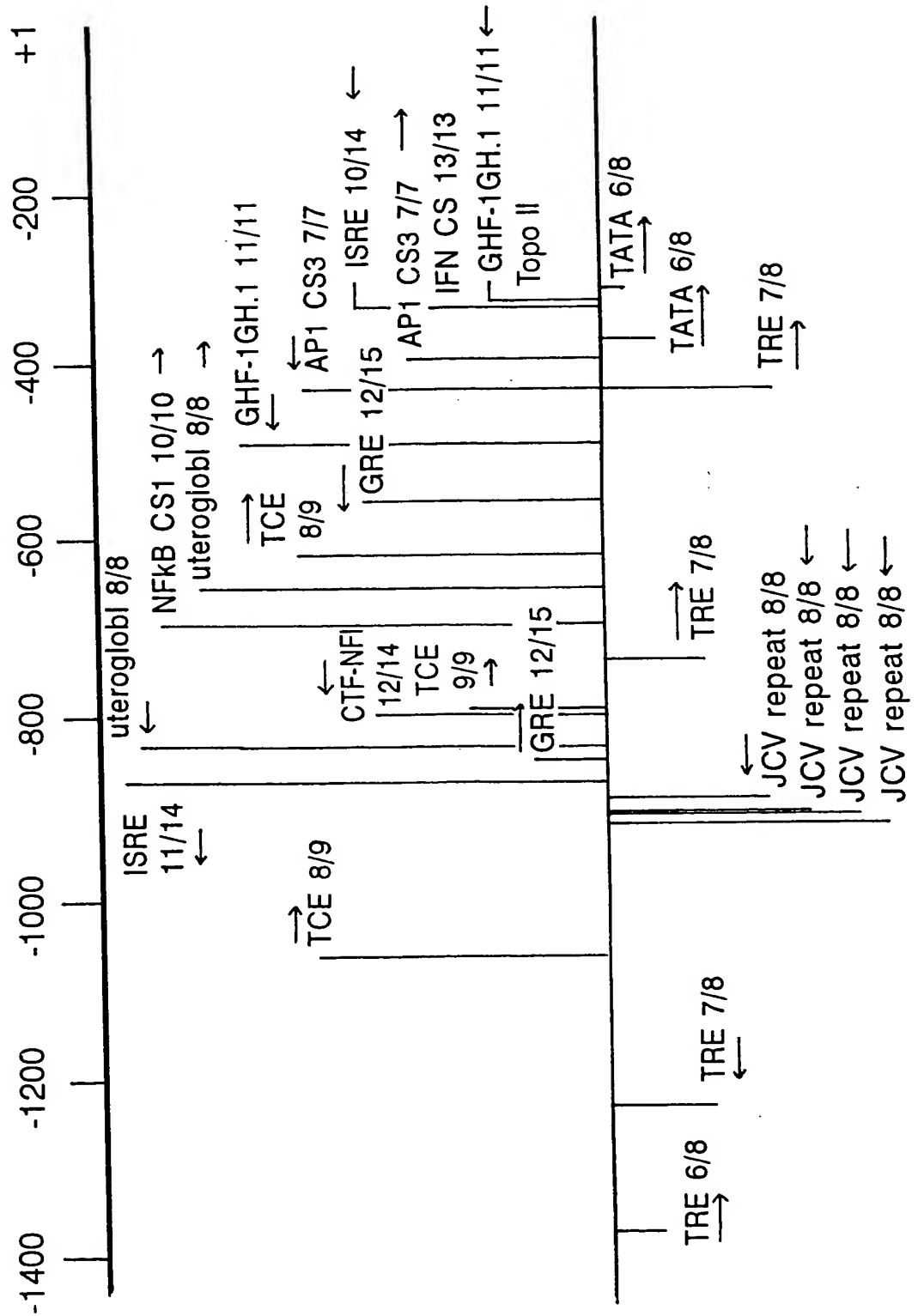


FIGURE 31

Prostate Specific Promoter: Cytosine Deaminase Chimera

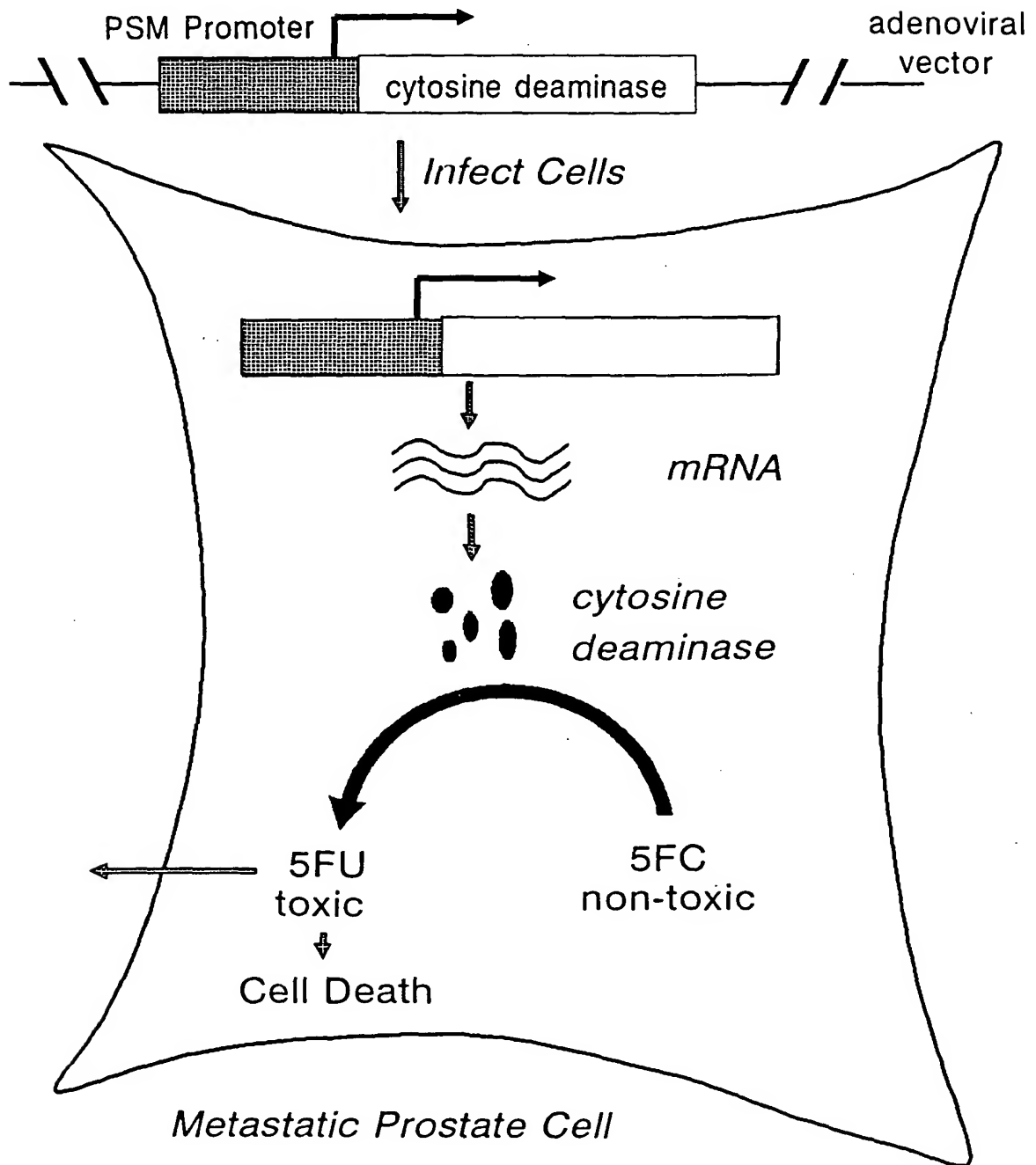


FIGURE 32A

	10	20	30	40	50	60
1	AAGGGTGCTC TTCCCACGAG	CTTAGGCTGA GAATCCGACT	ATGCTTGCAG TACGAACGTC	ACAGGATGCT TGTCCTACGA	TGGTTACAGA ACCAATGTCT	TGGGCTGTGA ACCCGACACT
61	CTCGAGTGGA GAGCTCACCT	GTTTTATAAG CAAAATATTCT	GGTGCTCCTT CCACGAGGAA	AGGCTGAATG TCCGACTTAC	CTTGCAGACA GAACGTCTGT	GGATGCTTGG CCTACGAACC
121	TTACAGATGG AATGTCTACC	GCTGTGAGCT CGACACTCGA	GGGTGCTTGT CCCACGAACA	AAGAGGATGC TTCTCCTACG	TTGGGTGCTA AACCCACGAT	AGTGAGCCAT TCACTCGGTA
181	TTGCAGTTGA AACGTCAACT	CCCTATTCTT GGGATAAGAA	GGAACATTCA CCTTGTAAGT	TTCCCCTCTA AAGGGGAGAT	CCCCTGTTTC GGGGACAAAG	TGTTCTGCCC ACAAGGACGG
241	AGCTAAGCCC TCGATTCTGGG	ATTTTTTCATT TAAAAAGTAA	TTTCTTTTAA AAAGAAAATT	CTCCTTAGCG GAGGAATCGC	CTCCGCAAAA GAGGCGTTTT	CTTAATCAAT GAATTAGTTA
301	TTCTTTAAAC AAGAAATTTG	CTCAGTTTTTC GAGTCAAAAG	TTATCTGTAA AATAGACATT	AAGGTAAATA TTCCATTTAT	ATAATACAGG TATTATGTCC	GTGCAACAGA CACGTTGTCT
361	AAAATCTAGT TTTTAGATCA	GTGGTTTACA CACCAAATGT	TAATCACCTG ATTAGTGGAC	TTAGAGATTT AATCTCTAAA	TAAATTATTT ATTTAATAAA	CAGGATAAGT GTCCTATTCA
421	CATGATAATT GTACTATTAA	AAATGAAATA TTTACTTTAT	ATGCACATAA TACGTGTATT	AGCACATAGT TCGTGTATCA	GTGGTGTCTT CACCACAGGA	CCATATAGAA GGTATATCTT
481	AATGCTCAGT TTACGAGTCA	ATATTGGTTA TATAACCAAT	TTAACTACTT AATTGATGAA	GTTGAAGGTT CAACTTCCAA	TATCTTCTCC ATAGAAGAGG	ACTAAACTGT TGATTTGACA
541	AAGTTCCACA TTCAAGGTGT	AGCCTTACAA TCGGAATGTT	TATGTGACAG ATACACTGTC	ATATTCATTC TATAAGTAAG	ATTGTCTGAA TAACAGACTT	TTCTTCAAAT AAGAAGTTTA
601	ACATCCTCTT TGTAGGAGAA	CACCATAGCG GTGGTATCGC	TCTTATTAAT AGAATAATTA	TGAATTATTA ACTTAATAAT	ATTGAATAAA TAACTTATTT	TTCTATTGTT AAGATAACAA
661	CAAAAATCAC GTTTTTAGTG	TTTTATATTT AAAATATAAA	AACTGAAATT TTGACTTTAA	TGCTTACTTA ACGAATGAAT	TAATCACATC ATTAGTGTAG	TAACCTTCAA ATTGGAAGTT
721	AGAAAACACA TCTTTTGTGT	TTAACCAACT AATTGGTTGA	GTACTGGGTA CATGACCCAT	ATGTTACTGG TACAATGACC	GTGATCCAC CACTAGGGTG	GTTTTACAAA CAAAATGTTT

FIGURE 32B

781	TGAGAAGATA	TATTCTGGTA	AGTTGAATAC	TTAGCACCCA	GGGGTAATCA	GCTTGGACAG
	ACTCTTCTAT	ATAAGACCAT	TCAACTTATG	AATCGTGGGT	CCCCATTAGT	CGAACCTGTC
841	GACCAGGTCC	AAAGACTGTT	AAGAGTCTTC	TGACTCCAAA	CTCAGTGCTC	CCTCCAGTGC
	CTGGTCCAGG	TTTCTGACAA	TTCTCAGAAG	ACTGAGGTTT	GAGTCACGAG	GGAGGTCACG
901	CACAAGCAAA	CTCCATAAAG	GTATCCTGTG	CTGAATAGAG	ACTGTAGAGT	GGTACAAAGT
	GTGTTCGTTT	GAGGTATTTT	CATAGGACAC	GACTTATCTC	TGACATCTCA	CCATGTTTCA
961	AAGACAGACA	TTATATTAAG	TCTTAGCTTT	GTGACTTCGA	ATGACTTACC	TAATCTAGCT
	TTCTGTCTGT	AATATAATTC	AGAATCGAAA	CACTGAAGCT	TACTGAATGG	ATTAGATCGA
1021	AAATTTTCAGT	TTTACCATGT	GTAAATCAGG	AAGAGTAATA	GAACAAACCT	TGAAGGGTCC
	TTTAAAGTCA	AAATGGTACA	CATTTAGTCC	TTCTCATTAT	CTTGTTTGGA	ACTTCCCAGG
1081	CAATGGTGAT	TAAATGAGGT	GATGTACATA	ACATGCATCA	CTCATAATAA	GTGCTCTTTA
	GTTACCACTA	ATTTACTCCA	CTACATGTAT	TGTACGTAGT	GAGTATTATT	CACGAGAAAT
1141	AATATTAGTC	ACTATTATTA	GCCATCTCTG	ATTAGATTTG	ACAATAGGAA	CATTAGGAAA
	TTATAATCAG	TGATAATAAT	CGGTAGAGAC	TAATCTAAAC	TGTTATCCTT	GTAATCCTTT
1201	GATATAGTAC	ATTCAGGATT	TTGTTAGAAA	GAGATGAAGA	AATTCCCTTC	CTTCCTGCCC
	CTATATCATG	TAAGTCCTAA	AACAATCTTT	CTCTACTTCT	TTAAGGGAAG	GAAGGACGGG
1261	TAGGTCATCT	AGGAGTTGTC	ATGGTTCATT	GTTGACAAAT	TAATTTTCCC	AAATTTTTC
	ATCCAGTAGA	TCCTCAACAG	TACCAAGTAA	CAACTGTTTA	ATTAAAAGGG	TTTAAAAAGT
1321	CTTTGCTCAG	AAAGTCTACA	TCGAAGCACC	CAAGACTGTA	CAATCTAGTC	CATCTTTTTC
	GAAACGAGTC	TTTCAGATGT	AGCTTCGTGG	GTTCTGACAT	GTTAGATCAG	GTAGAAAAAG
1381	CACTTAACTC	ATACTGTGCT	CTCCCTTTCT	CAAAGCAAAC	TGTTTGCTAT	TCCTTGAATA
	GTGAATTGAG	TATGACACGA	GAGGGAAAGA	GTTTCGTTTG	ACAAACGATA	AGGAACCTAT
1441	CACTCTGAGT	TTTCTGCCTT	TGCCTACTCA	GCTGGCCCAT	GGCCCCTAAT	GTTTCTTCTC
	GTGAGACTCA	AAAGACGGAA	ACGGATGAGT	CGACCGGGTA	CCGGGGGATTA	CAAAGAAGAG
1501	ATCTCCACTG	GGTCAAATCC	TACCTGTACC	TTATGGTTCT	GTAAAAGCA	GTGCTTCCAT
	TAGAGGTGAC	CCAGTTTAGG	ATGGACATGG	AATACCAAGA	CAATTTTCGT	CACGAAGGTA
1561	AAAGTACTCC	TAGCAAATGC	ACGGCCTCTC	TCACGGATTA	TAAGAACACA	GTTTATTTTA

FIGURE 32C

```

TTTCATGAGG ATCGTTTACG TGCCGGAGAG AGTGCCTAAT ATTCTTGTGT CAAATAAAAT

1621 TAAAGCATGT AGCTATTCTC TCCCTCGAAA TACGATTATT ATTATTAAGA ATTTATAGCA
      ATTTTCGTACA TCGATAAGAG AGGGAGCTTT ATGCTAATAA TAATAATTCT TAAATATCGT

1681 GGGATATAAT TTTGTATGAT GATTCTTCTG GTTAATCCAA CCAAGATTGA TTTTATATCT
      CCCTATATTA AAACATACTA CTAAGAAGAC CAATTAGGTT GGTTCCTAACT AAAATATAGA

1741 ATTACGTAAG ACAGTAGCCA GACATAGCCG GGATATGAAA ATAAAGTCTC TGCCTTCAAC
      TAATGCATTG TGTATATCGG CTGTATCGGC CCTATACTTT TATTTTCAGAG ACGGAAGTTG

1801 AAGTTCCAGT ATTCTTTTCT TTCCTCCCCT CCCCTCCCCT CCCTTCCCCT CCCCTTCCTT
      TTCAAGGTCA TAAGAAAAGA AAGGAGGGGA GGGGAGGGGA GGGGAAGGGGA GGGGAAGGAA

1861 CCCTTTCCCCT TCCCTTCCTT TCTTTCTTGA GGGAGTCTCA CTCTGTCACC AGGCTCCAGT
      GGGAAAGGGA AGGGAAGGAA AGAAAGAACT CCCTCAGAGT GAGACAGTGG TCCGAGGTCA

1921 GCAGTGGCGC TATCTTGGCT GACTGCAACC TCCGCCTCCC CGGTTCAAGC GATTCTCCTG
      CGTCACCGCG ATAGAACCGA CTGACGTTGG AGGCGGAGGG GCCAAGTTCG CTAAGAGGAC

1981 CCTCAGCCTC CTGAGTAGCT GGGACTACAG GAGCCCGCCA CCACGCCCAG CTAATTTTTG
      GGAGTCGGAG GACTCATCGA CCCTGATGTC CTCGGGCGGT GGTGCGGGTC GATTAAAAAC

2041 TATTTTTAGT AGAGATGGGG TTTCACCATG TTGGCCAGGA TGGTCTCGAT TTCTCGACTT
      ATAAAAATCA TCTCTACCCC AAAGTGGTAC AACCGGTCCT ACCAGAGCTA AAGAGCTGAA

2101 CGTGATCCGC CTGTCTGGGC CTCCCAAAGT GCTGGGATTA CAGGCGTGAG CCACCACGCC
      GCAC TAGGCG GACAGACCCG GAGGGTTTCA CGACCCTAAT GTCCGCACTC GGTGGTGCGG

2161 CGGCTTTAAA AAATGGTTTT GTAATGTAAG TGGAGGATAA TACCCTACAT GTTTATTAAT
      GCCGAAATTT TTTACCAAAA CATTACATTC ACCTCCTATT ATGGGATGTA CAAATAATTA

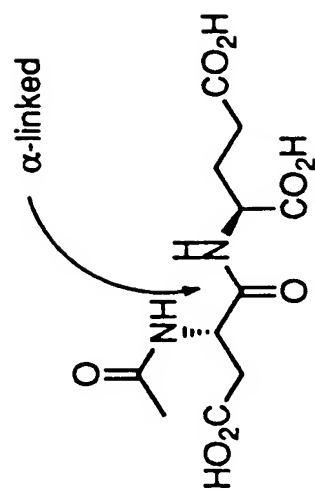
2221 AACATAATA TTCTTTAGGA AAAAGGGCGC GGTGGTGATT TACACTGATG ACAAGCATTG
      TTGTATTAT AAGAAATCCT TTTTCCCGCG CCACCACTAA ATGTGACTAC TGTTTCGTAAG

2281 CCGACTATGG AAAAAAGCG CAGCTTTTTT TGCTCTGCTT TTATTCAGTA GAGTATTGTA
      GGCTGATACC TTTTTTTCGC GTCGAAAAAG ACGAGACGAA AATAAGTCAT CTCATAACAT

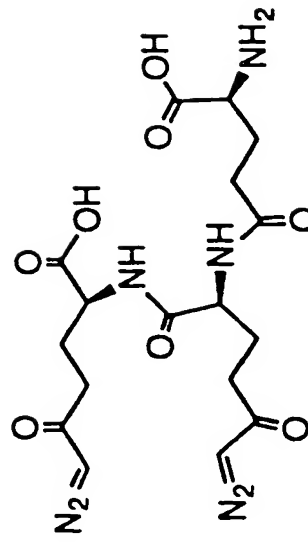
2341 GAGATTGTAT AGAATTTTCAG AGTTGAATAA AAGTTCCTCA TAATTATAGG AGTGGAGAGA
      CTCTAACATA TCTTAAAGTC TCAACTTATT TTCAAGGAGT ATTAATATCC TCACCTCTCT

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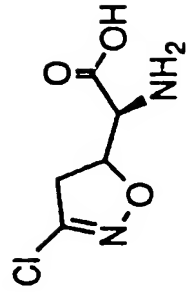
FIGURE 33



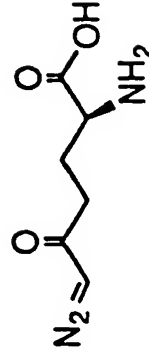
NAAG 1
N-acetylasparyl-L-glutamate



Azotomycin, becomes active by *in vivo* conversion to DON



Acivicin



6-diazo-5-oxo-norleucine, DON

FIGURE 34

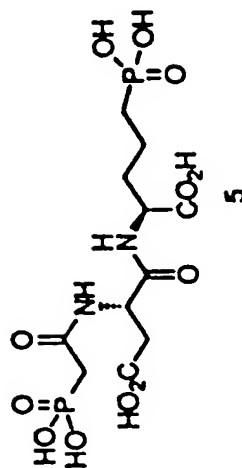
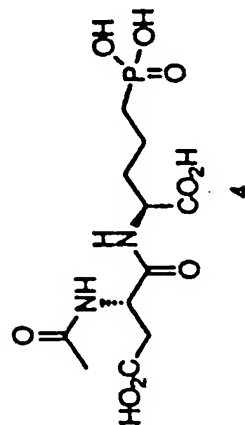
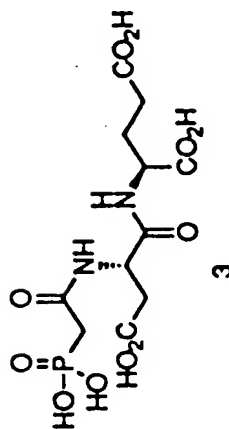
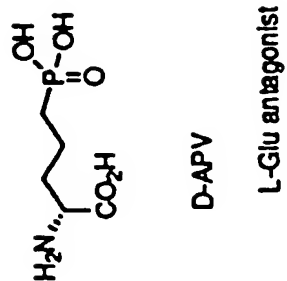
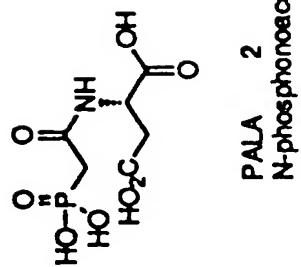
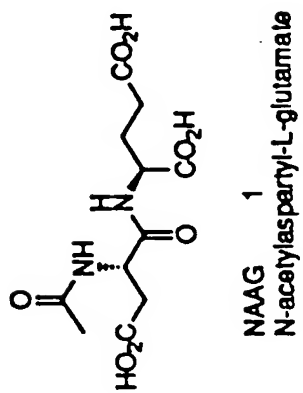


FIGURE 35

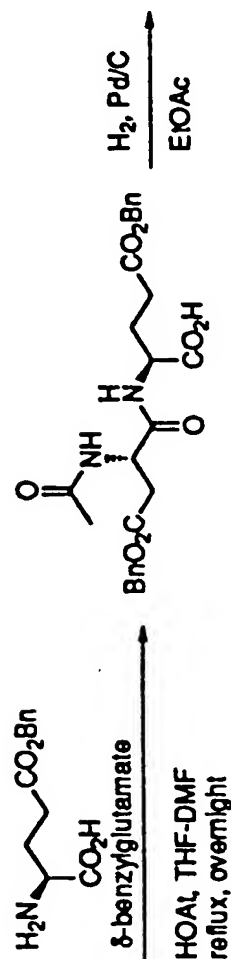
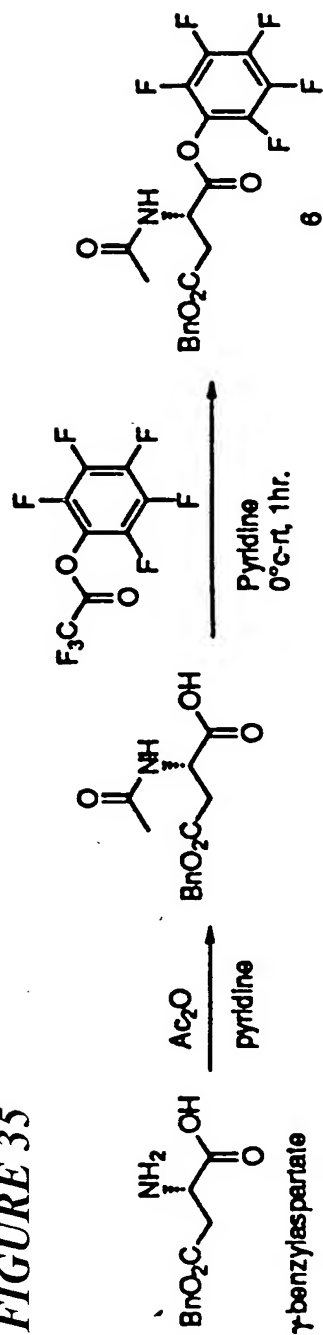


FIGURE 36

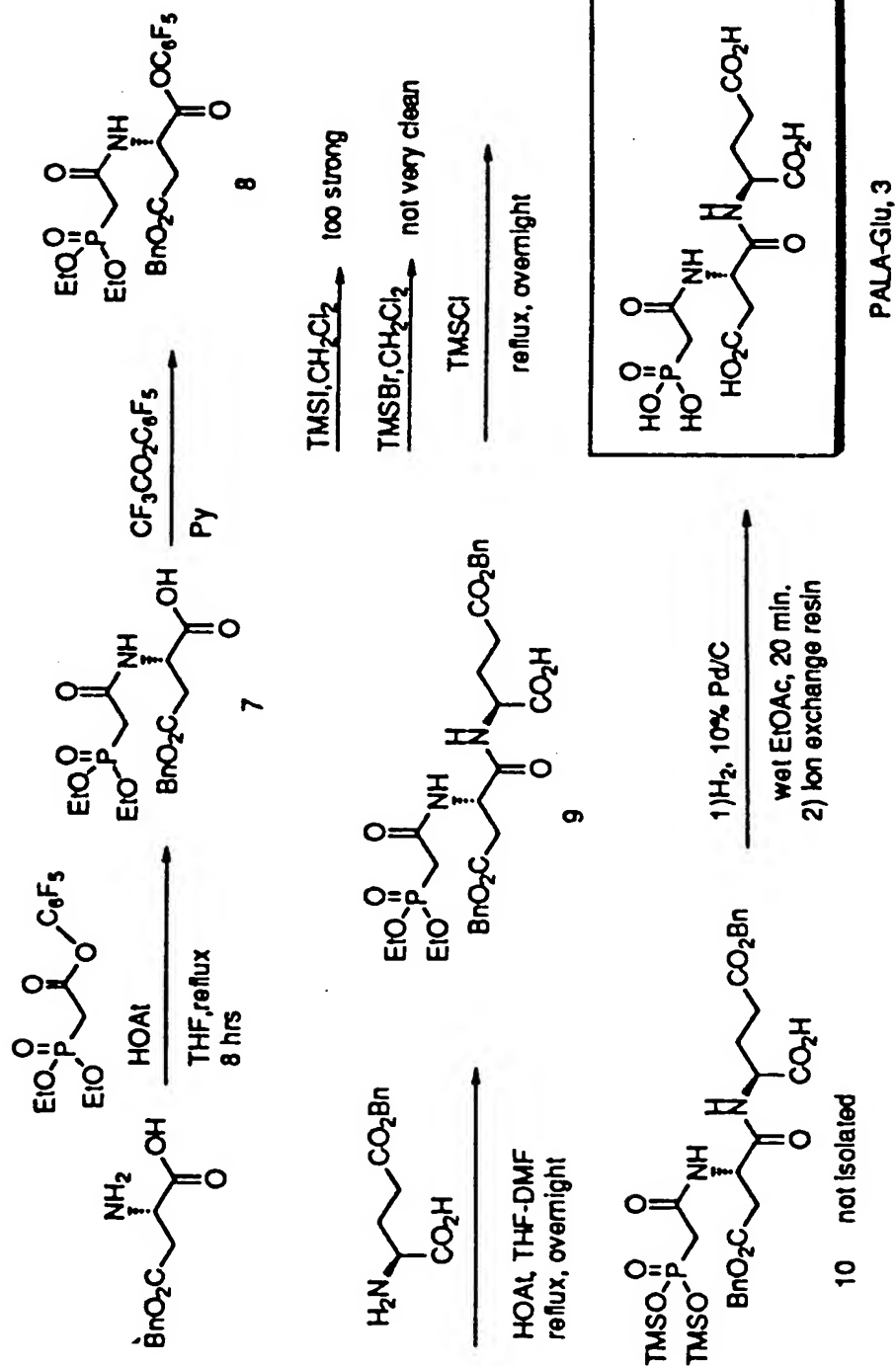


FIGURE 37

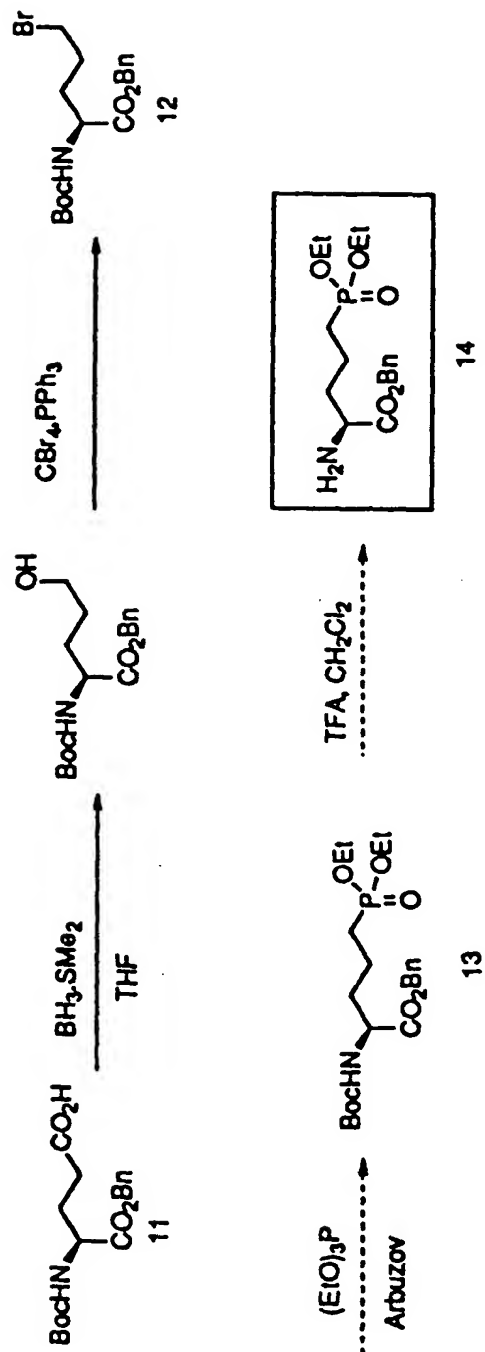


FIGURE 38

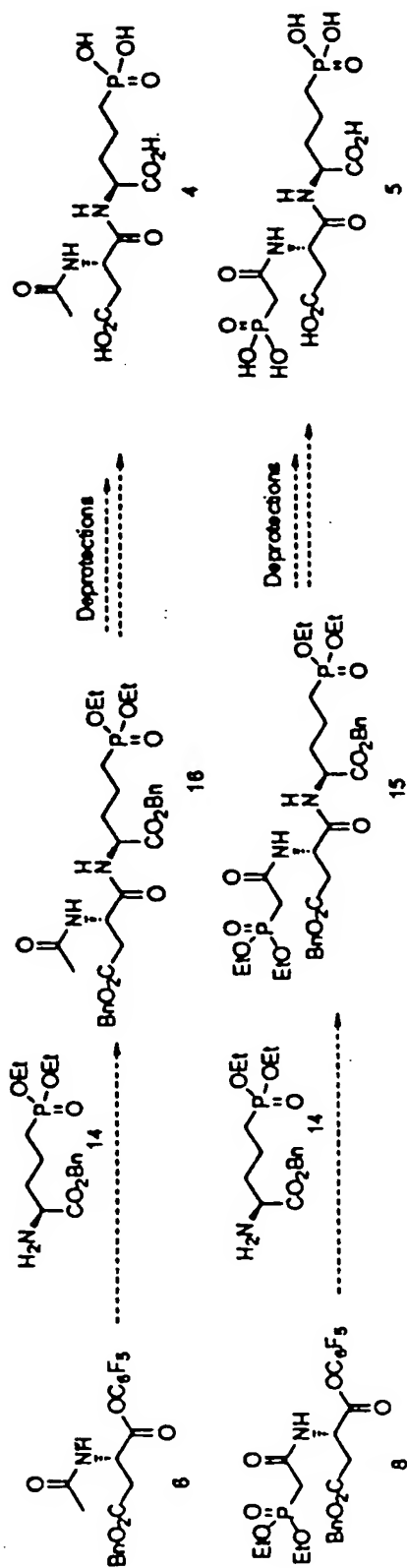
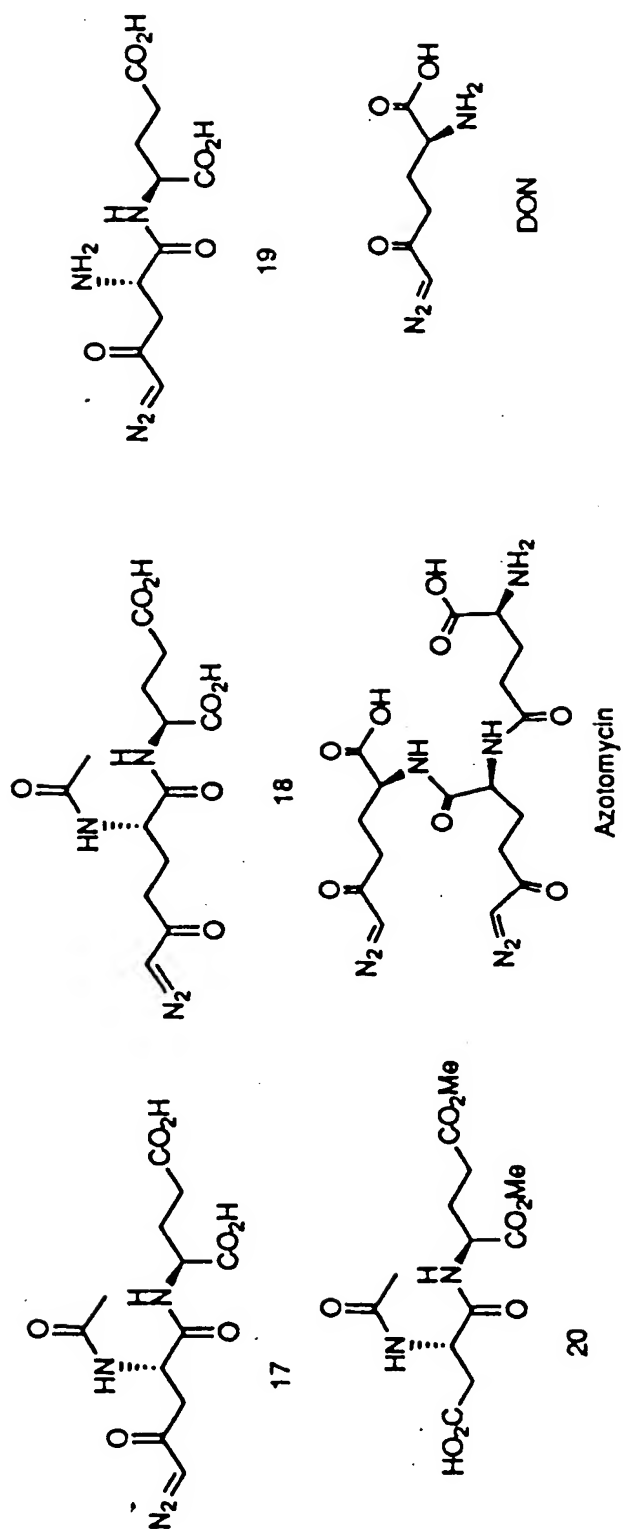


FIGURE 39



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FIGURE 40

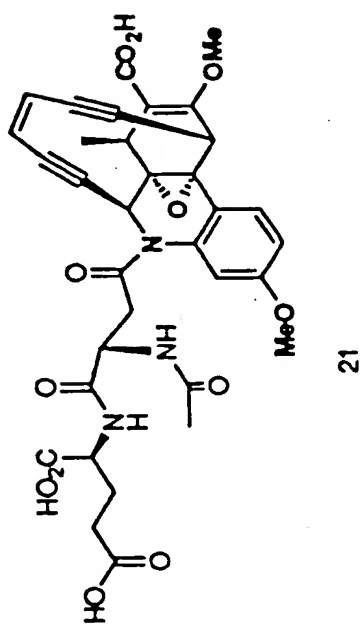
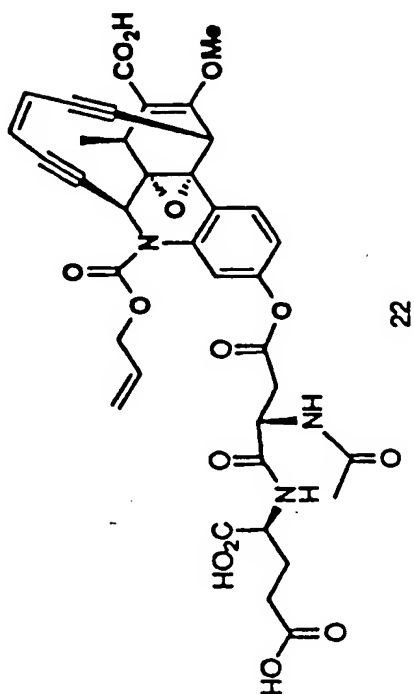
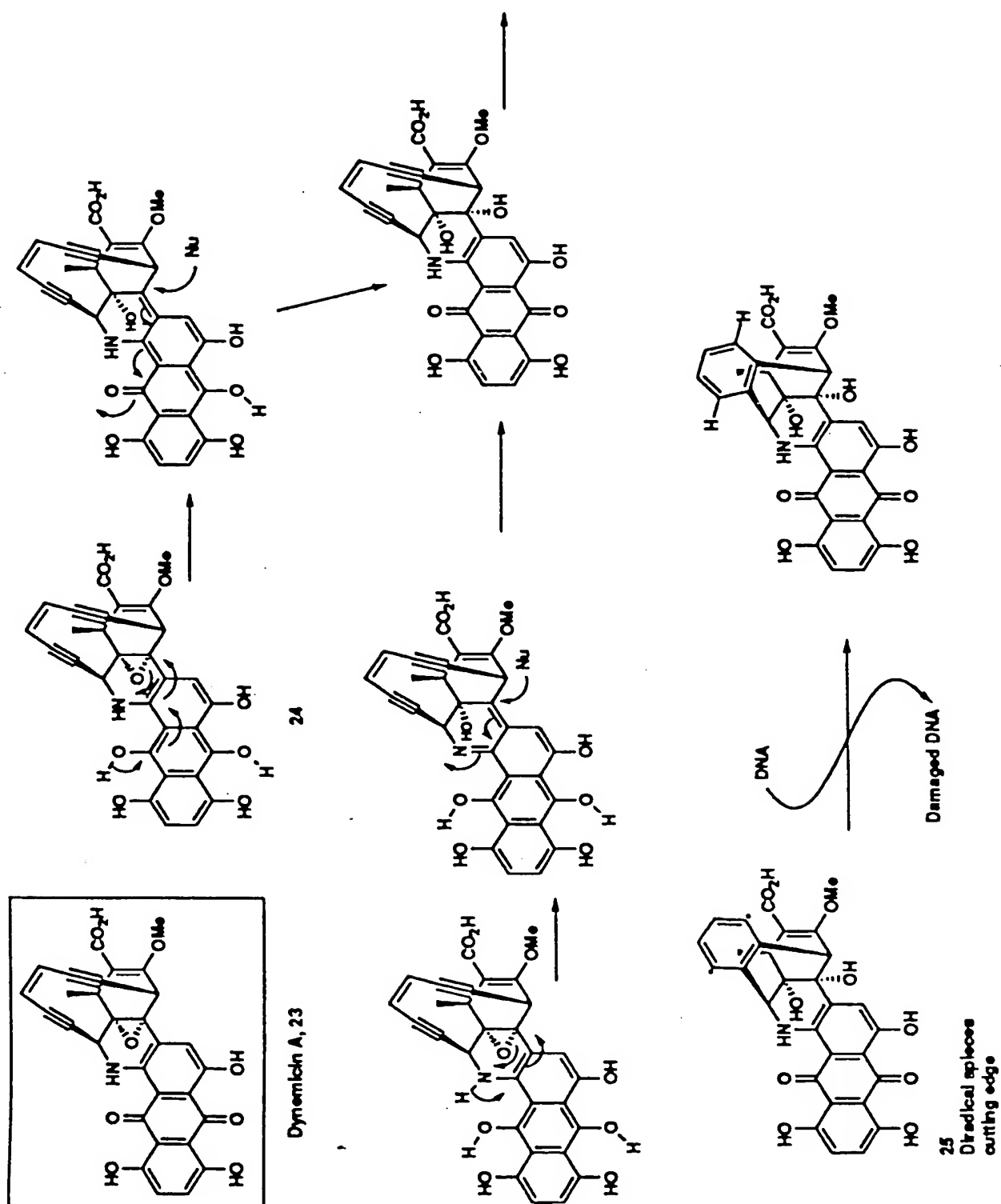
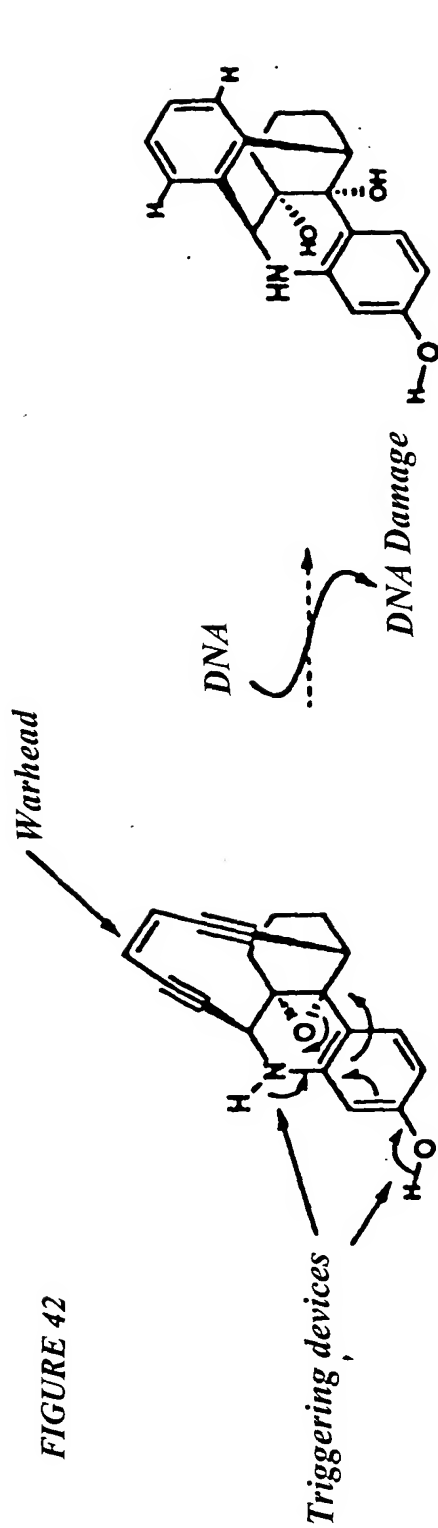


FIGURE 41





active at the nano to picomolar levels in different cell lines readily rearranges when one or both triggering devices are deprotected

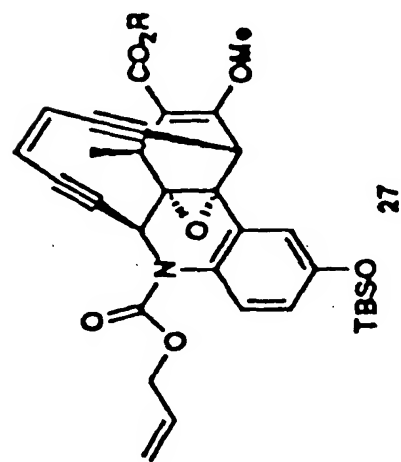
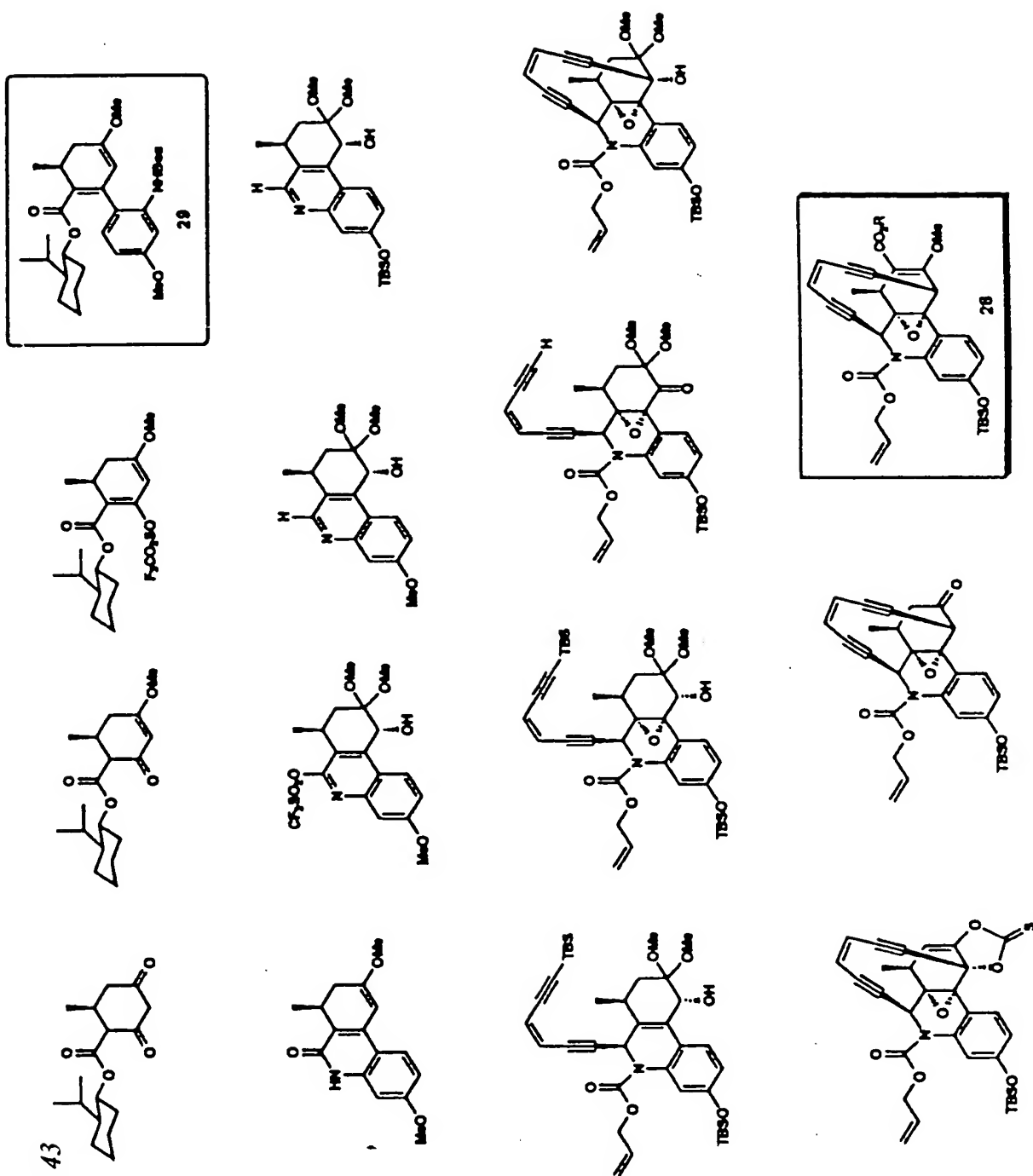


FIGURE 43



17 Steps for the optically active form 2

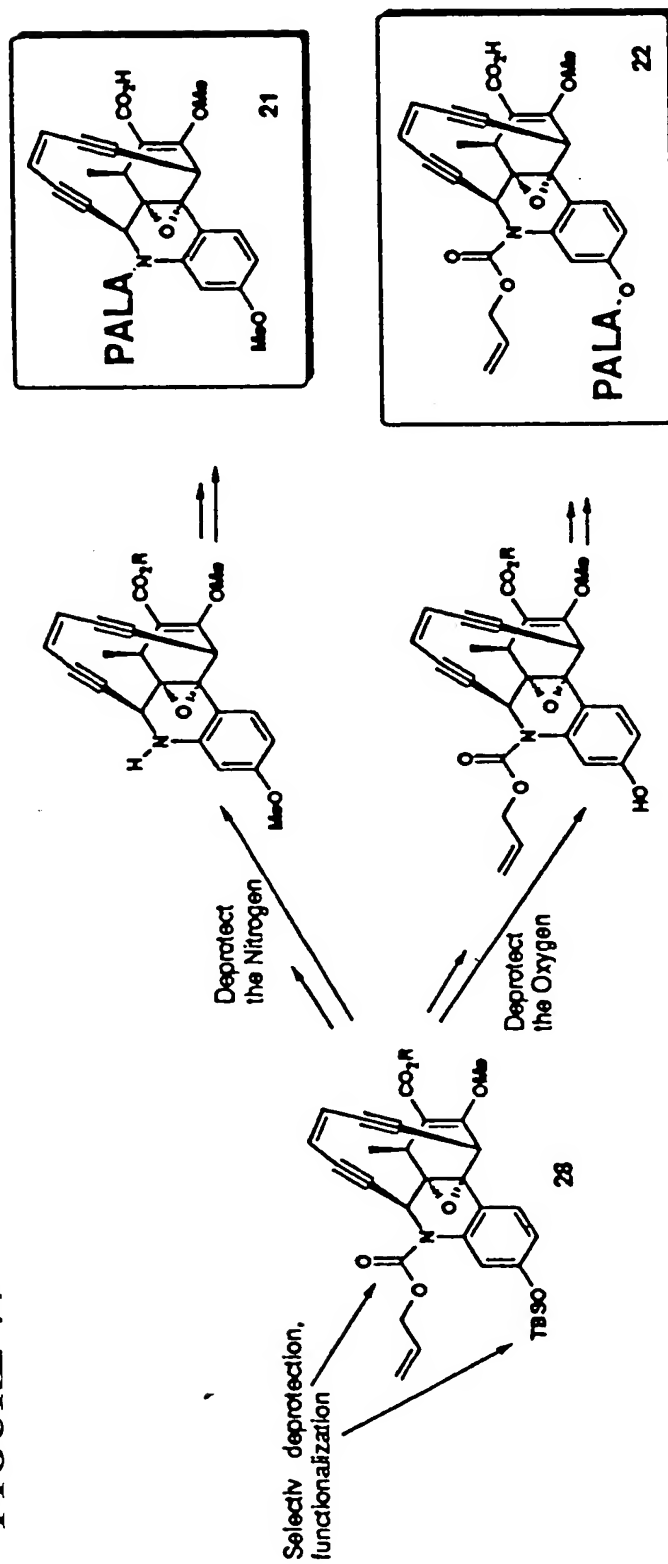


FIGURE 44

FIGURE 45

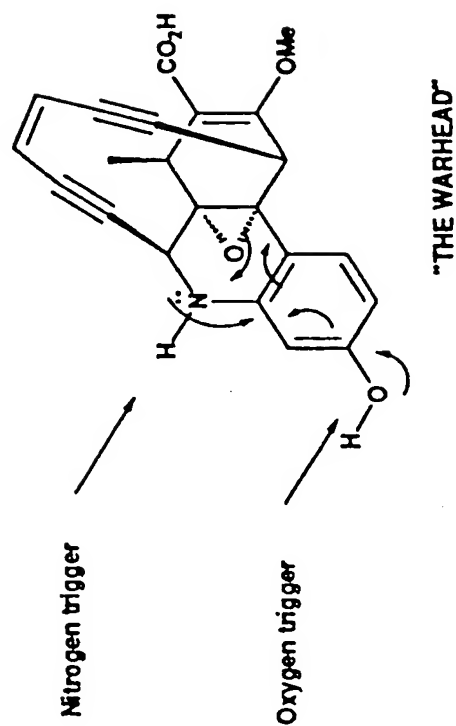
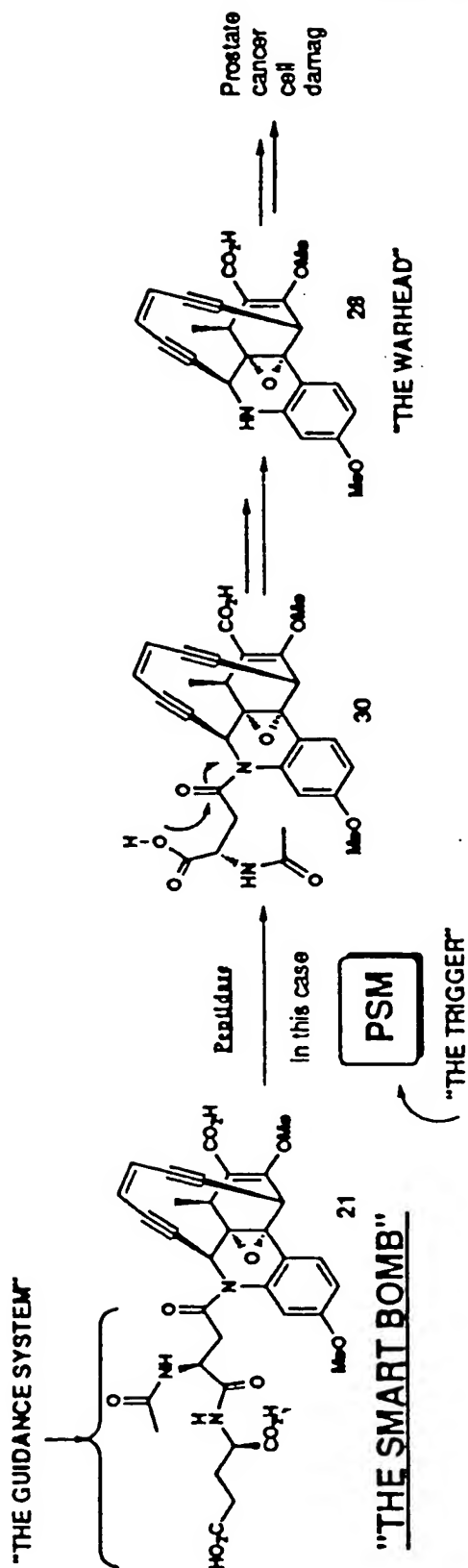


FIGURE 46A

	10	20	30	40	50	60
1	TAGGGGGCG	CCTCGCGGAG	AAACCTCGGA	GTCTTCCCCG	TGGTGCCGCG	GTGCTGGGAC
	ATCCCCCQC	GGAGCGCCTC	TTTGGAGCCT	CAGMAGGGGC	ACCACGCCGC	CACGACCCCTG
61	TCGCGGGTCA	GCTGCCGAGT	GGATCCTGT	TGCTGGTCTT	CCCCAGGGGC	GGCGATTAGG
	AGCGCCAGT	CGACGGCTCA	CCTAGGACA	ACGACCAGAA	GGGGTCCCG	CCGCTAATCC
121	GTGCGGGTAA	TGTGGGGTGA	GCACCCCTCG	ACTTAGGAGG	AGGTTAGCTG	GGAAACGGTGC
	CAGCCCCATT	ACACCCCACT	CGTGGGAGC	TCAATCCTCC	TCCCATCGAC	CCTTGCCACG
181	AGGGCTGAGT	TCTCACAAG	CTGCTGGTAG	GACAGTCACT	CAGGTTGAGG	GTAGAACTGA
	TCCCGACTCA	AGAGCTGTTC	GACGACCATC	CTGTCACTGA	GTCCAACTCC	CATCTTGACT
241	GAGAACCTGA	AACTGGGCGT	AGGAAGGTTT	CAAGTGCTGG	AGCCCTGCAA	GACAGAGGAA
	CTCTTGAGCT	TTGACCCGCA	TCCTTCCAAG	GTTACGACCC	TGGGACGTTT	CTGTCTCCTT
301	GTCTTTTCTT	TGCTTTTCTT	TTGTTTGT	TTGTTTGT	TTGTTTGT	TGTTTGT
	CAAAAATAAA	ACGAATAACA	ACAAAACAA	ACAAAACAA	ACAAAACAA	ACAAAACAA
361	TTTTTTTACC	TCTCTGTGCA	TTCTTTCTTC	CTTGGAAATA	ACAGAGGCAA	GCTTGGGAAC
	AAAAAATGG	AGAGACACGT	AAGAAGAAG	GAACCTTCAT	TGTCTCCGTT	CGAACCCCTTG
421	TGTTGTAACC	AGGTACAGCA	TCTGGACAGG	TCTTTACCAG	CGGGTCTTTT	GCTGTTTCTC
	ACACACTTGG	TCCAGTCGTT	AGACCTGTCC	AGAAATGGTC	GCCCAGAAJA	CGACAAJAAG
481	CTGGGTACTG	ATTGGCAGAC	TTGATCCAAC	TTTCTAAGAA	AAGCAGAAC	ACACAGGCAA
	GACCCATGAC	TAAAGGTCTG	AACTAGGTTG	AAAGATTCTT	TTCGTCTTGG	TGTGTCCGTT
541	GCTCAGACTC	TTTTATTAAA	TTCCAGTTTT	GACTTTGCCA	CTTCTTAGTG	GCCTGAAACA
	CGAGTCTGAG	AAATAATTT	AAGGTCAAAA	CTGAACCGT	GAAGAATCAC	CGGAACCTGT

FIGURE 46B

301 AGTTACCGAG TCCCTCTCAG CGTTAGTTAC CCTATTTTAT GATGAGGATA ATATTATCTG
 TCAATGGCTC AGGGAGAGTC GCAATCAATG GGATAAAATA CTACTCCTAT TATAATAGAC

 561 CAATTATTG GTAATAGTAA ATAATATAGC ATGTAATCT CCFAGCACAG TACTGGGATT
 GTTTAATAAC CATTATCATT TATTATATCG TACATTAGA GGATCGTGTC ATGACCCCTAA

 721 TTCOCCACTT TATTTCTTCT TTTACCAAGA TACTCCTCAT TGGACTTTAA TACACAGGAC
 AAGCGGTGAA ATAAAGAAGA AATCGTTCT ATGAGGAGTA ACCTGAAATT ATGTGTCCTG

 781 TAGTCTAAGG TATCACCAGG TAGTCCACTC CTGCTCGGAA TTCTTGACCC TCTTTCGGGA
 ATCAGATTCC ATAGTGTCC ATCAGGTGAG GACGAGCCTT AAGAACTGGG AGAAAGCCCT

 841 TTTAGAAGAA TAGGGCATGG ACCAGATGGG TTTAAACAAA TTCAATATCT TCCACTAGCT
 AAATCTTCTT ATCCCGTACC TGGTCTACCC AAATTGTGT AAGTTATAGA AGGTGATCGA

 901 TCACCTTGGG GTTGTTAAAA GATTTTIGAA CCACACACTG TGCTCATAAC AATCTTCATC
 AGTGGAAACCC CAACAATTT CTAAAAACTT GGTGTGTGAC ACGAGTATTG TTAGAAGTAG

 961 TCTTAAAGG ATTTTATCT TCCTGGTATT GCCCTCACTC TCATCCCTGT ATTCCGTGCT
 AGAATTTTCC TAAATAAGA AGGACCATAA CGGGAGTGAG AGTAGGGACA TAAGGCACGA

FIGURE 46C

1021 CAGTGGCTGA CACAGAAGAG TTCTTTATTG ATGTCCGCCC CCCACCCACT AGGATTCTCT
GTCACCGACT GTGTCTTCTC AAGAAATAAC TACAGGCGGG GGGTGGGTGA TCCTAAGAGA

1081 GCTCTCCCTT CCCCTACAG GCCTCCATCC TCTTCATCCT GTTCATTTT CAGATCTCAG
CGAGAGGGGA GGGGATGTC CGGAGTAGG AGAAGTAGGA CAAGTAAAA GTCTAGAGTC

1141 TTCAAGCATC TCGTCCCTCAG TGTGGTGTTC CCTGATCCCT CACTCTAATC CAAGTCTTTC
AAGTTCGTAG AGCAGGAGTC ACACCACAAA GGACTAGGGA GTGAGATTAG GTTCAGAAAG

1201 TGTTTTATGC ACAGGTGGAA TCTTATTTC GTTTGGCTCC AATCATGTAT TTTAATATGC
ACAAAATACG TGTCCACCTT AGAATAAAGG CAAACGCAGG TTAGTACATA AATTATATAG

1261 ATGTATATAT GTATGTGCAT TTGTATGCAT GCGATTAAAG ACTAGAATAA TTAATAATTG
TACATATATA CATACACGTA AACATACGTA CGCTAATICT TGATCTTATT AATTATTAAAC

1321 OAAAGCTCCA TGAAGCTGG TTGGGGACTA ATTTGTATC TACTTTATTC CCAGATCCTG
CTTTCGAGGT ACTTTCGACC AACCCTGAT TAAACATTC ATGAATAAAG GGTCTAGGAC

1381 TAATTCTCT AAATAAACCC TGGAACTCTG CCTATCTCC TTCAGGTTAA AAGCCAACTG
ATTAAAGAGA TTTATTGGG ACCTTAGAAC GGAATAGAGG AAGTCCAATT TTCGGTTGAC

1441 CAAAGTCTAA TGACTGCAGG ATCTAGCTAT CCAATTGTTT TGGCCGCCCTA TCGGTGCACT
GTTCCAGATT ACTGACGTCC TAGATCGATA GGTAAACAAAG ACCGGCCGAT ACGCACGTGA

1501 GGGTGTCTGG CAGAGAGGCT GGGTAAATTG TAGTTTCATT GTAGCTGTCT GACTTGGATT
CCCACAGACC GTCTCTCCGA CCCATTAAAC ATCAAGTAA CATCGACAGA CTGAACCTAA

1561 TCTCAGCCTT ACTTCACCTG AAACGCAAC TCTCACAGCA TTTTGTTTTA GTTTCAGAAAT
AGAGTGGGGA TGAAGTGACC TTTGCGTTTG AGAGTGTCGT AAACCAAAAT CAAAGTCTTA

1621 CAGAGCAAAAT TAGAAGTCTG AATTTCCTTC AACACTTGA AATAATTTAT TTATTTGAAA
GTCTCGTTA ATCTTCAGAC TTAAAGGAAG TTGTGAACCT TTATTAAATA AATAAACTTT

1681 TATATTGATA ATTAATTCCT TATAAAAATG TATTAATGC TTATTGAGT CAGCAGAGGA
ATATAAGTAT TAATTAAAGCA ATATTTTAC ATAATTAGG AATAAACTCA GTCGTCTCCT

FIGURE 46D

1741 AGATAGAAAC TTTATGAAAG TAGAAGGTGG ATCTCCTTTT TGCCTTCATT TTCAGAACAT
TCTATCTTTG AAATACTTTC ATCTTCCACC TAGAGGAAAA ACGGAAGTAA AAGTCTTGTA

1801 CTCGTTTACA CCCATTAGTT GAAACATTAA TGTCAATTTA TTTTCGTCCT GATTATCTCA
GAGCAAAATGT GGGTAATCAA CTTTGTAATT ACAGTAAAT AAAAGCAGGA CTAATAGAGT

1861 TAAACATTT CTTAGAATAA CAGCAATACC TATCATTTGAA GTTGGATAAG AAATATTTTG
ATTTTGTAAG GAACTCTTAT GTCGTTATGG ATAGTAACTT CAACCTATT CTTATATAAAC

1921 CAATTGGTTT GCAACTTAAA AATCTGTTTG CATGACTCTT TTTCAGTGAA AGTAGGCAAG
GTTAACCANA CGTTGAATTT TTAGACAAAC GTACTGAGAA AAGTCACTT TCATCCGTTT

1981 AGAAATTAAA ATTCAGAAAT ATCTCACCTA ATGTCAGAGG TAATATTGAT AATTGTGTT
TCTTTAATTT TAAGTCTTTA TAGAGTGGAT TACAGTCTCC ATTATAACTA TTAACACACA

2041 TTACAAATAA TACATACAAC AATAATGAAA AATAAGTCCT ATCTATAGOC TCGTATCTCA
AATGTTTATT ATGTATGTTG TTATTACTTT TTATTCAGGA TAGATATCCG AGCATAGAGT

2101 TGCCTATTTT TGGATGTATT TTTC
ACGGATAAAA ACCTACATAA AAAGT

FIGURE 47A

1	TGAAATAC	10	ATCAAAATA	20	GCATGACAT	30	ACGAGCCTAT	40	AGATAGGACT	50	TATTTTTTAT	60	TATTTTTTAT
	ACTTTTATG		TAGTTTTAT		CCGTACTCTA		TGCTCGGATA		TCTATCCTGA		ATAAAAATA		
61	TATTGTTOTA		TGTATTATTT		GTAACACAC		AATTATCAAT		ATTACCTCTG		ACATTAAGTG		
	ATACCAACAT		ACATAATAAA		CATTTGTGT		TAAATAGTTA		TAATGGAGAC		TGTAATCCAC		
121	AGATATTCTG		AATTTTAATT		TCTCTTGCCCT		ACTTTCACCTG		AAAAAGAGTC		ATGCAAAACAG		
	TCTATAAGAC		TAAAAATTAA		ACAGAAACGGA		TGAAAGTGAC		TTTTTCTCAG		TACGTTTGTC		
181	ATTTTAAAGT		TGCAAAACCA		TTGCAAAATA		TTTTTTTATC		CAACTTCAAT		GATAGGTATT		
	TAAAAATTCA		ACGTTTGGTT		AACGTTTAT		AAAAAAATAG		GTTGAAGTTA		CTATCCATAA		
241	GCTGTTAATT		CTAAGATATG		CATTAATTGT		TTCAACTAAT		GGGTGTCAAA		CGAGATGTTT		
	CGACAAATTAA		GATTCATATAC		GTAATTAAACA		AAGTTGATTA		CCCACAGTTT		GCTCTACAAG		
301	TGAAATGAA		GGCAAAAGG		AGATCCACCT		TCTACTTTCA		TAAAGTTTCT		ATCTTCCTCT		
	ACTTTTACTT		CGGTTTTCCT		TCTAGGTGGA		AGATGAAAGT		ATTTCAAAGA		TAGAAAGGAGA		
361	GCTGACTCAA		ATAAGCATTT		AATACATTTT		ATAACGAATT		AATTATGAAT		ATATTTCAAA		
	CGACTGAGTT		TATTCGTAAA		TTATGTAAAA		TATTGCTTAA		TTAATACTTA		TATAAAGTTT		
421	TAAATAAATT		ATTTCCAAGT		GTTGAAGGAA		ATTCAGACTT		CTAATTGCTT		CTGATTCTGA		
	ATTATTTTAA		TAAAGGTTCA		CAACTTCCTT		TAAGTCTGAA		GATTAACCGA		GACTAAGACT		

FIGURE 47B

481 AACTAAACA AATGCTCTGT GAGAGTTTGC GTTCCAGTG AAGTAGCGTG AGAAATCCAA
TTGATTTTGT TTACGAGACA CTCCTCAAACG CAAAGGTCAC TTCATCGCAC TCTTTAGGTT

541 GTCAGACAGC TACATGAAAC TACATTTACC AGCTCTCTGC CAGACACCAG TGCACGATAG
CAGTCTGTGG ATGTACTTTG ATGTAATGG TCGAGAGACG GTCTGTGGTC ACGTGCTATC

601 CGCAGAACAT GTAGCTAGAT CTCAGTCATA GCTNNNNNNN NNNNNNNNNN AGACCTTGCA
GCGTCTTGTA CATCGATCTA GAGTCAGTAT CGANNNNNNN NNNNNNNNNN TCTGGAAACGT

661 GTTGGCTTTT AACCTGAAGG AGATAAGGCA AGATCCAGG GTTTATTAG AGAAATTACA
CAACCGAAAA TTGGACTTCC TCTATTCCGT TCTAAGGTCC CAAATAAATC TCTTTAATGT

721 GGATCTGGGA ATAAAGTAGT TACAAAATTA GTCCCCAACC AGCTTTCATG GAGCTTTCAA
CCTAGACCCCT TATTTCATCA ATGTTTTAAT CAGGGGTTGG TCGAAAGTAC CTCGAAAGTT

FIGURE 47C

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781 TTATTAAATA TTCTAGTTCT TAATCGCATG CATACAATGC ACATACATAT ATACATGCAT
    AATAATTAAAT AAGATCAAGA ATTAGCGTAC GTATGTTAGG TGTATGTATA TATGTACGTA

841 ATTAATAATAC ATGATTGGAC GCAAACGGAA ATAAGAITCC ACCTGTGCAT AAAACAGAAA
    TAATTTTATG TACTAACCTG CGTTTGCCTT TATTCTAAGG TGGACACGTA TTTTGTCTTT

901 GACTTGGTTA GAGTGAGGGA TCAGGAAACA CCACACTGAG GACGAGATGN NNNNNNNNNN
    CTGAACCAAT CTCACTCCCT AGTCCTTTGT GGTGTGACTC CTGCTCTACN NNNNNNNNNN

961 NTAGTGGGTG GGGGGCGGAC ATCAATAAAG AACTCTTCTG TGTCAGCCAC TGAGCAGGGA
    NATCACCCAC CCCCCGCCG TAGTTATTTC TTGAGAAGAC ACAGTCGGTG ACTCGTGCCT

1021 ATAAAGGGAT GAGAGTGAGG GCAANTACCA GAAGAATAAA ATCCTTTTAA GAGATGAAGA
    TATTTCCTTA CTCTCACTCC CGTTNATGGT CTTCCTTATT TAGGAAATTT CTCTACTTCT

1081 TTGTTATGAG CACAGTGTGT GNTTCAAAA ATCTTTTAA CACCCCAAGG TOAAGCTAAT
    AACAACTACT GTGTCACACA CCNAACTTT TAGAAAATTG TTGGGGTTCC ACTTCGATCA

1141 TGGAAGATAT TTGAATTGTG TTAAACCCAT CTGGTCCTAG CCTATTCTT TGAATCCCGA
    ACCTCTATA AACTTAAACA AATTGGGTA GACCAGGATC GGGATAAGAA ACITAGGGCT

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FIGURE 47D

1201 AAGAGGGTCA AGAATTCCGA GCAGAGTGG ACTACCTGGT GATACCTTAG ACTAGTCCTG
TTCTCCCACT TCTTAAGGCT CBTCTCACC TGATGGAATC CTATGGAATC TGATCAGGAC

1261 TGTATTAAAG TCCAATGAGG AGTATCITGG TAAATAATA ATAAGAAGTCC CGAAATGCC
ACATAATTTC AGGTTACTCC TCATAGAACCC ATTATATTAAT TTATTTTCAGG GCTTTTAGGG

1321 AGTACTGTGC TAGGAGATTI ACATGCTATA TTATTTACTA TNNNNNNNNT AATTGCAGA
TCATGACACG ATCCTCTAAA TGTACGATAT AATAAATGAT AHHNNNNNNNA TTAACACOTCT

1381 TAATATTATC CTCATCAATA AATAGGGTAA CTACGCTGA GAGGACTCG GTAACCTTGT
ATTATAATAG GAGTAGTATT TTATCCCAAT GATTGCGACI CTCCTGAGC CATTGAACAA

1441 CAAGGCCACT AAGAAGTGGC AAGTCAAAA CTGGAATTT AATAAAGAG TCTAGCTTGC
GTTCCGGTGA TTCTTCACCG TTICAGTTTT GACCTIAAA TTATTTTCTC AGATCGAAGC

1501 CTGTGTGGTT CTGCTTTTCT TAGAAAGTTG GANNAAGTCT CANATCAGTA CCCAGGAAAA
GACACACCAA GACGAAAAGA ATCTTTCAC CTNNTTCAGA GTTAGTCAT GGGTCCCTTT

1561 ACAGCAAAG ACCCGCTGGT AAAGACCCTGT CCAGATTGCT GACCTGGTTC ACACANHTCC

FIGURE 47E

TGTCGTTTTC TGGCGACCA TTCTGGACA GGTCTAACGA CTGGACCAAG TGTGTRNAGG

1621 AAGCTTGCCT CTGTTACTTC CAAGGAAGAA AGAATGCACA GAGAGGTAAA AAAACAACA
TTCGAACGGA GACAATGAAG GTTCCTTCIT TCCTACGTGT CTCGCCATTT TTTTGTTTGT

1681 AACCAACAA AACAAACAA AACAAACAA AAGCAAAAA AACCTTCCTC
TTGGTTTGT TTGTTTGT TTGTTTGT TTGTTTGT TTGTTTGT TTTGAAGGAG

1741 TGTCTTGCAG GGCTCCAGCA CTTGGAACCT TCCTACGTCC TANTTTCAGG TTCCTCAGT
ACAGAACGTC CCGAGGTCGT GAACCTTGA AGGATGCAGG ATNAAGTCC AAGAGAGTCA

1801 TCTACCCCTCA ACCTGAGTGA CTGTCCTACC AGCAGCTTGT CGAGAAGTCA GCCCTGCACC
AGATGGGAGT TGGACTCACT GACAGGATGG TCGTCGAACA GCTCTTGAST CGGACCGTGC

1861 GTTCCCAGCT ACCCTCCTCC TAACTCGAGG GGTGCT
CAAGGCTCGA TGGAGGAGG ATTGAGCTCC CCACGA

FIGURE 48A

1	GGATTCGTGTT	GAGCCCTAGC	TCATTATGAT	GTCCGTGTTGT	CCTACCCAAA	TAAGACTCAT
	CCTAAGACAA	CTCGGGATCG	AGTAATACTA	CAGGACAACA	GGATGGGTTT	ATTCTGAGTA
61	CCCAACTACA	TCTCAATAAT	TAATGAAGAT	GGAATGAGG	TAAAAAATMA	ATAAATAAAT
	GGGTTGATGT	AGAGTTATTA	ATTACTTCTA	CCTTACTCC	ATTTTATT	TATTTATTTA
121	AAAGAAACA	TTCCCCCCCCA	TTTATTATTT	TTTCAATAC	CTTCTATGAA	ATAATGTTCT
	TTTTCTTTGT	AAGGGGGGT	AAATAATAAA	AAAGTTATG	GAAGATACTT	TATTACAAGA
181	ATCCCTCTCT	AAATATTAAT	AGAAATCAAT	ATTATTGGAA	CTGTGAATAC	CTTTAATATC
	TAGGAGAGAA	TTTATAATTA	TCTTTAGTTA	TAAATACCTT	GACACTTATG	GAAATTATAG
241	TCATTATCCG	GTGTCAACTA	CTTTCCTATG	ATGTTGAGTT	ACTGGGTTTA	GAAGTCGGGA
	AGTAATAGGC	CACAGTTGAT	GAAAGCATAC	TACAACTCAA	TGACCCCAAAT	CTTCAGCCCT
301	ATAATGCTG	TAAANNNNNN	AGTTAGTCTA	CACACCAATA	TCAAATATGA	TATACTTOTA
	TTATTACGAC	ATTTNNNNNN	TCAATCAGAT	GTGTGGTTAT	AGTTTATACT	ATATGAACAT
361	AACCTCCAAG	CATAAAAGA	GATACTTTAT	AAAAGAAGTT	CTTTTITCT	TTTTTTTTTT
	TTGGAGGTTT	GTATTTTCT	CTATGAATA	TTTCTCTCAA	GAAAAAAGA	AAAAAANA

FIGURE 48B

421 TCCAGATGGA GTTTCACCTC TGTCAGGCGA GCNAGTGCA GTGGTGCCAT CTCGGCTCAC
 AAGTCTACCT CAAAGTGAGG ACAGTCCGTC CGNCTCACGT CACCACGGTA GAGCCGAGTG

481 TGCAACCTCC ACCTCCCATG TTCAAGGGAAT TCTCCTTCCT CAGTCTCCTG AATAAGCTGGG
 ACGTTGGAGG TGGAGGGTAC AAGTTCCCTA AGAGGAAGCA GTCAGAGGAC TCATCGACCC

541 ATTACAGGTG TGCACCACCA CACCCAGCTA ATTTTGTAT TTTTAATAGA GACAGGGTTT
 TAATGTCCAC ACGTGGTGGT GTGGGTGAT TAAACATA AATAATTATCT CTGTCCCAAA

601 CATCGATGTT GGCAGGCTA GTCTCGAAT CCTGACCTCT AGGTGATCCA CCCGGCTCAG
 GTAGCTACAA CCGGTCCGAT CAGAGCTGA GAACTGGAGA TCCACTAGGT GGGCGGAGTC

661 CCTCCCCAAG TTGTAGAAAT ACACGTGTGA GGCACGCTC TGGCCAGGAG ATACATTTT
 GGAGGGTTTC AACATCTTAA TGTGCACACT CCGTGACGAG ACCGGTCCCTC TATGTAAAAA

721 GATAGGTTTA ATTTATAAAG ACACTGCACA GATTGGAGT TGTGGGAAA TCACGATCCA
 CTATCCAAAT TAAATATTTC TGTGACGTGT CTAAACCTCA ACGACCCCTT AGTGCTAGGT

FIGURE 48C

781 GTATGCATTT GACCCAGCAA TTTTATTGG TACTTAATGA TTATAICTCA ATTGATCAGG
CATACGTAAA CTGGTCGTT AAAATAACC ATGAATTACT AATATAAGT TAACTAGTCC

841 TTGAACCTCG TGCAGAGAT TTGTGTGTTG ACATTTGAGA GGACAGTTTQ GAGGCAAGGT
AACTTGAGAC ACGCTTCTA AACACACACC TGTAACCTCT CCGTCAAAC CTCCTTCCA

901 ATTTTAGTAG ATTAAAGAA TTTGAATCTT GTTGCNAGT TGGGCAATAT ACTGAGMAAG
TAAATCATC TAAATTCTT AAAGTTAAG CAAACCTTCA ACCCGTATA TGACTCTTTC

961 AAGAGACAAT GCAGATAAAT TGATATATTT ATTATGATGT ATGTTCAATA TGAAGATCA
TCTTCTGTTA CGTCTATTTA ACTATATAAA TAATACTACA TACAAGTTAT ACTTCTTAOT

1021 CAAATATAA CATACATNNA TCTTACTTAA CATACCTCAG TTTTAGAGGT ACCGTATCTA
GTTTATATTT GTATGTANNT AGAATONATT GTATGAGAGC AAAATCTCGA TGGCATACAT

1081 GAAGAGTCCA TTTCTATTTA GGTAACTTCC TTTAGTCCTT TTATTACTGQ GCACCTCTAA
CTTCTCAGGT AAGATNAAT CCATTCNAGG AAATCAGGAA ANTAIGACC COTGAGAAAT

1141 TTACATGTAG CTTGAATAT GTCCAGTTTG AGCAGTGNAC TGAANIGTC ATGTGATTA
AATGTACATC GAACTTTATA CAGGTCAAAC TCGTCACCTG ACTTTTACAG TACACTAAT

1201 GTACATATAT AATTTTTTT CATAGTAGGT CAATAACCTC CTTTATTGA CTAAATGAATC
CATGTATATA TTAAAAAAA GTATCATCCA GTTATTGGAG GAAATATACT GATTACTTAG

1261 AGTTCTCTAA TGATTATACG
TCAAGAGATT ACTAATATGC

FIGURE 49A

1	AATCAAAATA	10	AAACAGTTAA	20	AGTTTGATTA	30	CTATAATCAA	40	ACACAAAATA	50	AATGAATATT	60	
	TTAGTTTTAT		TTTGTCAAAT		TCAAACATAAT		GATATTAGTT		TGTGTTTTTT		TTACTTATAA		
61	ATCTTTTATG		TCAGTAGAGG		GTAAATGAAT		CCTTCAGGAT		TTTGATGATA		GTATCAGATA		
	TAGAAAATAC		AGTCATCTCC		CACTTACTTA		GGAAGTCCTA		AAACTACTAT		CATAGTCTAT		
121	CCCAGCACTA		TGCTAGAAGT		TGTGAAGAAT		TCACGAGATG		AATAAATCAC		AGATTCTGTC		
	GGGTCGTGAT		ACGATCTTCA		ACACTTCTTA		AGTGCTCTAC		TTATTAGTGT		TCTAAGACAG		
181	CTCAAAATGG		TTAGATCTAT		TCAGGAAACA		AAGCTAAAAA		AACCCACCCA		ATAACTAAAA		
	GAGTTTACC		AATCTAGATA		AGTCCTTTGT		TTCGATTTTT		TIGGGGTGGT		TATTGATTTT		
241	ATCAACCMAA		TGAAAAACAA		CAATCATAAA		ATAAGTAAGT		ACCTATAGAA		AGAAAAGCTC		
	TAGTTGGTTT		ACTTTTGTGT		GTTAGTATTT		TATTCATTCA		TGGATACTCT		TCTTTTCGAG		
301	AGAGGAGGTA		AAAAGATAAC		TCTTCCAAAA		GGAATACTAT		AIACGTAAAA		CTGTGTACTG		
	TCTCCTCCAT		TTTTCTATTG		AGNAGGTTTT		CCTEATGATA		TATGACATTT		GACACATGAC		
361	ATAGAAGGAA		GAATTAGAAA		NNNNNNNNNTG		TAAGTGGCAT		ACATACTAAG		CTAGTGTGAA		
	TATCTTCCTT		CTTAATCTTT		NNNNNNNNNAC		ATTCACCGTA		TGTATGATTC		GATCACACTT		

FIGURE 49B

421 CACAAGCCCTA AATATGTAGT TGCTTCACAG AAGGTTAGAA GTAAATTAACT CTCATGAATT
GTGTTCCGGAT TTATACATCA ACGAAGTGTC TTCCAATCTT CATTTAATTG GAGTACTTAA

481 TCCTGAGAGA ACTTGTAAGG ACTAAGCTTT CGATTTTGGG GAAAGATTTT AATACCAAAAT
AGAACTCTCT TGAACATTCC TGATTGMAA GCFAAAACCT CTTTCIAAAA TTATGGTTTA

541 AAAAAGTACC TTTGTTTGGT AATCTCAATC ATTATAATAG TGCTTAGATA ATACCTAGGA
TTTTTTCATGG AAACAACCA TTAGAGTTAG TAAATATTATC ACGAATCTAT TATGGATCCT

601 ACAAAATTAA TATTAAATTT ACTTTAAAAA AAAGTACATG ATTGGGGAAAT CACAACCTGGC
TGTTTAATTT ATAATTTAAA TGAAATTTTT TTTCATGTAC TAAACCCCTTA GTGTTGACCG

661 CTTACTAGAT TCTCTNNNNN NATATGCACT GAAAGAATG AAAACACCTG AACCAATAT
GAATGATCTA AGAGANNNNN NTATACGTGA CTTTICTTAC TTTTGTGAC TTGGTTTATA

721 NTGTTTTTTT AAGTTTAAAA TTAAATTGGA AAAAATAGT AAGGAATATC AGNAGCAAAA
NACAAAAAAA TTCAAATTTT AATTTAACCT TTTTITTATCA TTCCTTATAG TCCTCGTTTT

FIGURE 49C

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781 AAATAAATG AAAGCAAGAA TCCTCAGAGG TAGCACGAAA TTTGGCTTTG CTTAGATGGA
   TTTATTTTAC TTTCGTTCTT AGGAGTCTCC ATCGTGCTTT AAACCGAAAC GAATCTACCT

841 TCTATCAAAAG CTAATGGCCCA TGAAGAAGAT TCAGGAGTTA GTTTAAAGCT GGTTCACATA
   AGATAGTTTC GATACCGGGT ACTTTTCCTA AGTCCTCAAT CAAATTTTGA CCAAGTGTAT

901 ATGGAATCTA GCAGAAGACT GTGCATAAAG GTGGTCTAAG AACAAACAATA TCCTGACCAG
   TACCTTAGAT CGTCTTCTGA CACGTATTTC CACCAGATTTC TTGTTGTTAT AGGACTGGTC

961 GTGAGGGGGC TCACNCTNAA TNCCAGCACT TTGGAGGCCC AAGTGGGTG GATCACCAAG
   CACTCCCCCG AGTGNGANTT ANGGTCGTGA AACCCTCGGG TTCCACCCAC CTAGTGCTCC

1021 TCAGGAGTTT GAGACCAGCC TGACCAACAT GGTGAAACCG CGTCTCTACT AAAAATAGAA
   AGTCCTCAAA CTCTGGTCGG ACTGGTTGTA CCACTTTGGC GCAGAGATGA TTTTATCTTT

1081 AAATTAGCCG NGCCTACGTG CTTCTAATCC CAGCTGAACT CAGGAGACTG AGACAGGAGA
   TTTAATCGGC NCGGATGCAC GAAGATTAGG GTCGACTGA GTCCCTCTGAC TCTGTCTCT

1141 ATCACTTGAA CCCAGCATGC AAGCTTNNNN NNGCCACTGC ACTCCAGCCT AGGGTGCAAA
   TAGTGAACTT GGGTCGTAGG TTCGAANNNN NNCGGTGACG TGAGGTGGA TCCCACGTTT

1201 AAAAAAAAA ANGACACATT ACTCAGGTAA GGTAATCAAT AA
   TTTTTTTTTT TNCGTGTAA TGAGTCCATT CCATTAGTA TT

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FIGURE 50A

[illegible]

FIGURE 50B

|||||
- A T T T A A A A A T T C C C T T T C G A C T G T A G A C A A A T A G G A A T T T G G C C T G T -
- G G G T C T A C T T G C T T A T T A T A T T T G T A A G C T A G T G G T A G G A A A T A G C A A A -
- G G G T C T A C T T G C T T A T T A T A T T T G T A A G C T A G T G G T A G G A A A T A G C A A A -
- T G C T C A C T A C C A C T A A T A A G A A C A T T T C T A A A T C T G A T G T T C T G A G G A T T -
- T G C T C A C T A C C A C T A A T A A G A A C A T T T C T A A A T C T G A T G T T C T G A G G A T T -
- T T T A G A G C T T A T A G T A G C A A A A G A A A A G G G A A A T T C T A T C C G A G A T G T C -
- T T T A G A G C T T A T A G T A G C A A A A G A A A A G G G A A A T T C T A T C C G A G A T G T C -
- C T T T G T T G T A G G C C T A A T G A G A A A A G G T T G A G A T A A A G T T C T G G T A C T C -
- C T T T G T T G T A G G C C T A A T G A G A A A A G G T T G A G A T A A A G T T C T G G T A C T C -
- A T T T A A G T G T A A T A T T G A A A A T T G A T A T T A C C G A A T C T G G A A C A A C C A A T -
- A T T T A A G T G T A A T A T T G A A A A T T G A T A T T A C C G A A T C T G G A A C A A C C A A T -
- T T A A A A T A A G G A A A G A A G A C A C T G T G T T T T C T -
- T T A A A A T A A G G A A A G A A G A C A C T G T G T T T T C T -

FIGURE 51A

	10	20	30	40	50	60
1	AGAAACACAC TCTTTTGTGT	GTGTCCTTTCT CACAGAAAGA	TTCCCTTAATTT AAGGAATAAA	TAAATTGGTT ATTTAACCAA	GTTCCAGATT CAAGGTCTAA	CGTAATATC GCCATTATAG
61	AATTTTCAAT TTAAAAAGTA	ATTACACCTTA TAATGTGAAT	AATGAGTACC TTACTCAIGG	AGAACTTTAT TCTIGAAATA	CTTCAACCCTT GAACTTGGAA	TTCTCATTAG AAGAQTAAATC
121	GCCTACAAAC CGGATGTTGT	AAGGACATCT TTCCTGTAGA	CGGATAGAAT GCCATCTTA	TTCCCTTTTC AAGGAAAAAG	TTTTTGGCTAC AAAAACGATG	TATAAGCTCT ATATTCCGAGA
181	AAAAATCCTC TTTTTTAGGAG	AGAACATCAG TCTTGTTAGTC	ATTAGAAAT TAAATCTTTA	GTCTTTATTA CAAGAATAAT	GTGGTAGTGA CACCATCACT	GCATTTGCTA CGTAAACGAT
241	TTTCTCTACCA AAAGGATGGT	CTAGCTTACA GATCGAATGT	AATAAATAA TTATATTATT	GCAAGTAGAC CGTTCATCTG	CCCACAGGCC GGGTGTCCGG	AAATTCCTAT TTTAAGGATA
301	TTGTTCTACA AACAAAGATGT	GTGAAAGGG CAGCTTTCCC	AATTTTTTAA TTAAAAAATT	AATTTAATTT TTAAATTAAA	CCCACATAAG GGGTGATTTC	AGAAAAATAT TCTTTTTATA
361	ATTAACAAAT TAATTGTTTA	CAAATGACAG GTTTACTGTC	TAATTTTTAA ATTAATAAAT	ATTGCTATG TAAACGATAC	TGTAATTTGT ACATTTAACA	TTTCCCTCAT AAAGGGAGTA
421	TATTTATAAC ATAAATATTG	AATTCATACT TTAAGTATGA	ACAAATTAAT TGTAAATTA	TTAGIAAACA AATCATTTGT	TTTTTGTAGA AAAAACATCT	AAATATTTAA TTTATANAAT

FIGURE 51B

481 AACAAAGATA CTGAAAGTTA ATATNAAACC CAGTGCATGC TTCTTGTAGG CCACAGCCAT
TTGTTTCTAT GACTTTCAAT TATANTTTGG GTCACGTACG AAGAACATCC GGTGTCGGTA

541 AACCTGTAAG CACAGAAAAA TTTGTTCTGT TACTCTAAAC ATCTACACIG GCCAAATTCC
TTGOACATTC GGTCTTTT AAACAAGACA ATGAGATTG TAGATGTGAC CGGTTTAAGG

601 AATGCTCGAA TTTAACCCCG GGATATAACC TAGTAAATGT GTCCTCTCTG TAAGGTGGCG
TTACGAGCTT AAATTGGGGC CCTATATTGG ATCATTTACA CAGGAGAGAC ATTCCACCCG

661 ATGTCACAGA ATACAAGAA ATAATGGTAT TCATAAACTT TTAAGAAAT GATTCTACAC
TACAGTGTCT TATGTTCTTT TATTACCATA AGTATTTCAA AATTCTTTA CTAAGATGTG

721 ATGTAAACC CACTATAACT TTTTACATTG GGGGAGACAA AAAAGAGAT AATTTTACC
TACATTTTGG GTGATATTGA AAATGIAAC CCCCTCTCTT TTTTCTCTA TTAATAATGG

781 TT
AA

FIGURE 52A

1	GATGCTATTT	10	GGGCAATTTC	20	TTATTGACAG	30	TTTTGAAATG	40	TTAGGCTTTT	50	ATCTCCATTT
	CTACGATAAA		CCCGTTAAAG		AATAACTGTC		AAACITTTAC		AATCCGAAAA		TAGAGGTAAG
61	TTIAGTACTT		AAATTTTCCA		ACATGGGTGT		TGCTTGTTAT		TTATCAGTA		TAAAAAAGAA
	AAATCATGAA		TTTAAAGGT		TGTACCCACA		ACGAACAATA		AAATAGTCAT		ATTTTATCTT
121	GAGTGGTTCT		GTTCTGGAAT		TTAGTATATA		CATGAGTATC		TAGTGTATGT		CAGCCATGAA
	CTCACCAAGA		CAAGACCTTA		AATCATATAT		GIACTCATAG		ATCACATACA		GTCGGTACTT
181	AATGAACCTT		TCAGATGTTT		AACCTCAGGG		AACCTAATTG		AGTCATTGCT		CCAGACATTG
	TTACTTGGAA		AGTCTACAAA		TTGAGAGTCCC		TTGGATTAAAC		TCAGTAACGA		GGTCTGTAAAC
241	TTGCTTTGAA		CCCACTATAT		TNNNNNNNCT		CGGGCAATGA		CTCAGTGTGG		CAAGGATACT
	AACGAAACTT		GGGTGATATA		ANNNNNNNGA		GCCCGTTACT		GAGTCACACC		GTTCCTATGA
301	ACTGCAGGCC		TGTTTCTGGA		AGGCACIGGA		CTCCTCTGAT		GCAAACTTTG		GCCAGGGACT
	TGACGTCCGG		ACAAAGACCT		TCCGTGACCT		GAGGAGACTA		CGTTTGAAAC		CGGTCCCTGA
361	CCTTGATAGC		TCTTAAATAG		ATGCTGCACC		AACACTCTCT		TTCTTTTCTC		TCTTTTCTTT
	GGAACTATCG		AGATTATTATC		TACGACGTGG		TTGTGAGAGA		AAGAAAAGAG		AGAAAAGAAA

FIGURE 52B

421 TATTCAATAT TAGACTACAA GCAGTCTAAG GACTTCTCAG GTTTCTAGC TCTCTCTCAT
ATAAGTTATA ATCTGATGTT CGTCAGATTC CTGAAGAGTC CCAAGATCG AGAGAGAGTA

481 TTCACACATG CTTTCCTAGT AATCTCTACT CAIATATCTT ACTGCTACGC TGGGGCCAGA
AAGTGTGTAC GAAAGGATCA TTAGAGATGA GTATATAGAA TGACGATGCG ACCCCGGTCT

541 TAACNNNNNN CTTCCATTTT GTTTTATCT CTATCTCTT TCCCCTCTG CTTTCATTAT
ATTGNNNNNN GAAGGTAA ACAAATAGA GATAAGAAGA AGGGGAGAC GAAATATATA

601 TGAAACTTTC TGCTTTCATT ATTGAAACTT TCCCAGATT GTTCTGCTTA ACCTGGCATT
ACTTTGAAAG ACGAAAGTAA TAACTTTGAA AGGGTCTAAA CAAGACGAAT TGGACCGTAA

661 GGAACGTGTT CCTCTTCCCT GTGCTGCTTT CTCCCATGCG CATGTCCTTT TTTTCTTTT
CCTTGACAAA GGAGAAGGA CACGACGAAA GAGGGTAACG GTACAGGAAA AAAAAA

721 TTTTTTTTTT TGAGACAGTG TCACTCTGTT GCCCAGGCTG GAGTCAATG GTGCAATCTT
AAAAAATA ACTCTGTCAC AGTGAGACAA CGGGTCCGAC CTCACGTAC CACGTTAGAA

FIGURE 52C

781 GCCCACTGCA ACCCCGCGCT CCGGGGTYCA AGTGATTCTC CTGCTCAGC CTCCTGAGTA
CCGGTGACGT TGGGCGCGGA GGCCCAAGT TCACTAAGAG GACCGAGTCG GAGGACTCAT

841 GCTGGGATTA CAGGTGCCCA CCACTATGCC CGGCTGATTT TTGTATTTT AGTAGAGATN
CGACCCTAAT GTCCACGGGT GGTGATACGG GCCGACTAA AACATAAA TATCTCTAN

901 NNNNNNNTTT CACCATNGCT GATCAGGCTG GTCTCGAACT CCTGACCGCA GTGANTCCGC
NNNNNNNAAA GTGGTANCGA CTAGTCCGAC CAGAGCTTGA GGACTGGCGT CACTNAGGCG

961 CCTCCTTGCC CTCCCNAAGT GCTGACATTA CAGGCATGAG TCACTGCGNC CAGCCACCAT
GGAGGAACCG GAGGGTTTCA CGACTCTAAT GTCCGTACTC AGTGACCGNG GTCGGTGATA

1021 TATTCTCTAG AGGTGAGAGA ACACGTGGCTC TTCTAACAG TTGAATTTG ATAGAGACC
ATAAGAGATC TCCACTCTCT TGTGACCGAG AAGATTGTTT AACTTTAAAC TATCTCTGO

FIGURE 53A

1	CACAAATAAA	GATTATTAGC	CACAAATAAA	CCTTGAAGTA	ACGCATTAA	ATGTTAATGG
	GTGTTTTTTT	CTAATAATCG	GTGTTTTTTT	GGAATTTCAT	TGCGTAATTT	TACAATTACC
61	ATTCACTTTA	TTGAOCATCT	GCTCATAATA	CTTAAATGAG	TGCMAAGTGC	TTTGAATATA
	TAAGTGAAT	AACTCGTAGA	CGAGTATTAT	GAAATTACTC	ACGTTTCACG	AAACTTATAT
121	ATACGTCATT	TAAACCTTAC	CATAATTTCG	AGGAA'TTGCT	ACCTCCACTT	CACAGATGGG
	TATGCAGTAA	ATTTGGAATG	GIATTAAGAC	TCC'TTAACGA	TGGAGGTGAA	GTGTCTACCC
181	GCACAGGAGG	CTTAGATAAC	ATGCCCAAG	TCATGCTTCT	AGTAAATGGA	TATAATTAAAG
	CGTGCTCCTC	GAATCTATTG	TACGGGTTTC	AGTACGAAGA	TCATTTACCT	ATATTAAATTC
241	ATTCAAATTA	TTGATAAGAA	TTTGATCTGC	CTTACCAGTA	TCTAGTAGTA	AATCTAAAG
	TAAGTTTAAT	AACTATTCTT	AAACTAGACG	GAATGGTCAT	AGATCATCAT	TTAGATTTTC
301	CGCTTTCCAG	AGCATGTGCT	GTGATAGAG	CTTGATGCT	AACTCTCTGA	AATTTCCAT
	GGAAAGGTC	TCGTACACGA	CAACTATCTC	GAACTACAGA	TTGAGAGACT	TTAAAGGTA
361	TCTTATTGTT	CTCACTGGTA	TATAGTTATT	TTTTACTACT	TTCATACACC	TACTAAGAAAG
	AGAATAAACA	GAGTGACCAT	ATATCAATAA	AAATGATGA	AAGTATGTGG	ATGATTCTTC

FIGURE 53B

421 ACAGGAGGAT CAAAGATAGG ATTTCAATTA GAATGCCCTAA AGCTTCACGT ATTTAATTC
TGTCTCCTTA GTTCTATCC TAAAGTAAAT CTTACGGATT TCGAAGTGCA TAAATTAAG

481 AGAATAAGAT TCAGGCAGAC CACCAGTATA TGCCATGGTC CCTGGTTATC TTTCAGCAGG
TCTTATTCTA AGICCGTCTG GTGGTCATAT ACGGTACCAG GGCCTAATAG AAAGTCGTCC

541 TGACCGAGAA AGAAACATG GTAATGTITA TGAATGCTG GGTCTTGTG GTTTCACCTC
ACTGGCTCTT TCTTTGTAC CATTACAAAT ACTTIACCAC CCAAGAACAT CAAAGTGAAAG

601 AACATATCTG CCTTTACIGT ATTAAGATGA TGGATTAACT TATTCTTGAT ATGGGCATGT
TTGTATAGAC GGAATGACA TAATICTACT ACCTAATTGA ATAAGAACTA TACCCGTACA

661 AAAACAATAT ACTTTTACTA AACAGCTACA GAGAGACAA TGTGTTTCCA GACAACTTA
TTTTGTATA TGAATAATGAT TTGTCGATGT CTCCTGTGTT ACACAAAGGT CTGTTTGAAT

721 AGAGACTGAG TGTTCAAACT GAATAATCTC GACCTTAATT GTAACATAT TTTATGAAAT
TCTCTGACTC ACAAGTTTGA CTTATTAGAG CTGGAATTAA CATGATATA AAATACTTAA

FIGURE 53C

781 CCAGCTGTAA GCCAAAACA GACTTCTTTG GGCCTACCAC GGCATTTTG TTCCTGTTAN
 GTCGACATT CCGTTTGT CTGAAGAAC CCGGATGGTG CCCGTAAAC AAGGACAAATN

 841 NNNTACTCCA AACCTTAAC CCACGTCCAC TTAATAAAG GCCTGGAAT AAATGTCATT
 NNNATGAGGT TTGGAATTG GGTGCAGGTG AATTATTAC CGGACCTTA TTACAGTAA

 901 ATCTGATATT ATACTGAGAT GTTTAGTTAT GAAATCAAA GTGGAGAATT TCAATCTGTC
 TAGACTATAA TATGACTCTA CAAATCAATA CTTAGTTT CACCTCTTA AGTTAGACAG

 961 CTGTAAGCTT TCTCTGCCGT CACGACCCTC ATGCACTCAG GCTGTGCGGT GCAGCATGCT
 GACATTGAA AGAGACGCCA GTGCTGGAG TACGTGAGTC CGACACGCCA CGTCGTACCA

 1021 CTGTCATGTC TGTTTTCTTC TGCCGTGTACA CGGGTGGTG TTCCTGTCTA CCTGTTTGAG
 GACAGTACAG ACAAAAGAAG ACGGACATGT GCCCACCAC AAGGACAGAT GGACAACTC

 1081 GAAATATGAA TACGTNNNN NCTAGAATCT ACTGCACATG CAATAAGGA ACAATCAGTA
 CTTTATACTT ATGCANNNN NGATCTTAGA TGACGTGTAC GTTATTCCTT TGTTAGTCAT

 1141 AGAATCACTT TCTCGTGGAA AATTCATTAG AATTAACATC TCGTTTTAA ATGCTCTATC
 TCTTAGTGAA AGAGCACCTT TTAAGTAA'IC TTAATTGTAG AGCAAAATTT TACGAGATAG

FIGURE 53D

1201 AAGTGTAAG TAATTCCTCT CTCTTTTCCC TTTTTCACIA AGGAGTTTGT ATATTAAACA
TTTCACATTT ATTAAGGAGA GAGAAAGGG AAAAGTGAT TCCTCAACA TATAATTGT

1261 GAATTTCAG TAATGTATTA TAAATTATT TAANNATTT ACAATAAAT GCCACGTATA
CTTAAAGTTC ATTACATAAT ATTTAAATAA ATTNATAAA TGTATTTTA CGTGCAATAT

1321 AGCATCAAGC AACATGANNN NNNCATTTGGT AGAAGCACA ATACATAGTC AAACAGCAG
TCGTAGTTCC TTGTACTNNN NNGTAACCA TCTTTCGTGT TATGTATCAG TTTTGTCTGC

1381 AGTATTAAAT AACAGAAAA TTTGCAAAAG GCAAGTAAG AATATACATA TACTTAATTA
TCATAAATTA TTTGTCTTTT AAACGTTTC CGTTCATTTC TTATATGTAT ATGAATTAAAT

1441 TACATAAAAT ATTGATACAG GAGGTAGAAA GAAATTTAAT AAGCAGATAA TGGGGGCAAC
ATGTATTTTA TAACTATGTC CTCCATCTTT CTTTAAATCA TTCGTCTATT ACCCCCGTTG

1501 AGAGTCCTCA GCAGAGCTTC CCTTCTAACA AAAAGCAGCC CAATAAATTA TTTTTTTTTT
TCTCAGGAGT CGTCTCGAAG GGAAGATTGT TTTTCGTCCG GTTATTTAAT AAAAAAAAAA

1561 CTAACAAAA GCAGCCTGAA AAATCGAGCT GCAACATAG ATTAGCAATC GGCTGAAAGT

FIGURE 53E

GATTGTTTTT CGTCGGACTT TTAGCTCGA CGTTGTATC TAATCGTTAG CCGACTTTCA

 1621 GCGGGAGAAAT OCTGGCAGCT GTGCCAATAG TAAAGGGCTA CCTGGAGCCG GCGCGGTGGC
 CGCCCTCTTA CGACCGTCGA CACGGTTATC ATTTCCCGAT GGACCTCGGC CCGCGCACCG

 1681 TCACGCTGTA ATCCCAGCAC TTTGGGAGGG CGAGGCAACG CGGATCACCT GAGTCGGGA
 AGTGGGACAT TAGGGTCGTG AAACCTCCG GCTCCGTTGC GCCTAGTGGG CTCCAGCCCT

 1741 GTTTGAGATC AGCCCGACCA ACATGGAGAA ACCCCGTCTC TACTAAAAA AAAAAAAA
 CAAACTCTAG TCGGGCTGGT TGTACCTCTT TGGGGCAGAG ATGATTTTTT TTTTTTTTTT

 1801 AAAGGC AAAA ATGAGCCGG GCATGGTGGC ACATGCCCTTG CACATCCCAG CTGAGGCAGG
 TTTCCGTTTT TTA CTCTGGCC CGTACCACCG TGTACGGAAC GTGTAGGGTC GACTCCGTCC

 1861 AGAATTCACT TGAACCTGGG AGGTAGAGAT TCGGGTGAAG CGAGATCAGC TCATTGCACT
 TCTTAAGTGA ACTTGGACCC TCCATCTCTA ACGCCACTTC GCTCTAGTGC AGTAACGTGA

 1921 CCAGCCCTGGG CAAAAGAGC AAACTTAGT CTCAAAAA AAANNCAA GAAAAA
 GGTCCGACCC GATTTTCTCG TTTTGAATCA GAGTTTTTTT TTTTNNGTTT CTTTTTTT

FIGURE 54

Genomic Organization of PSM Gene

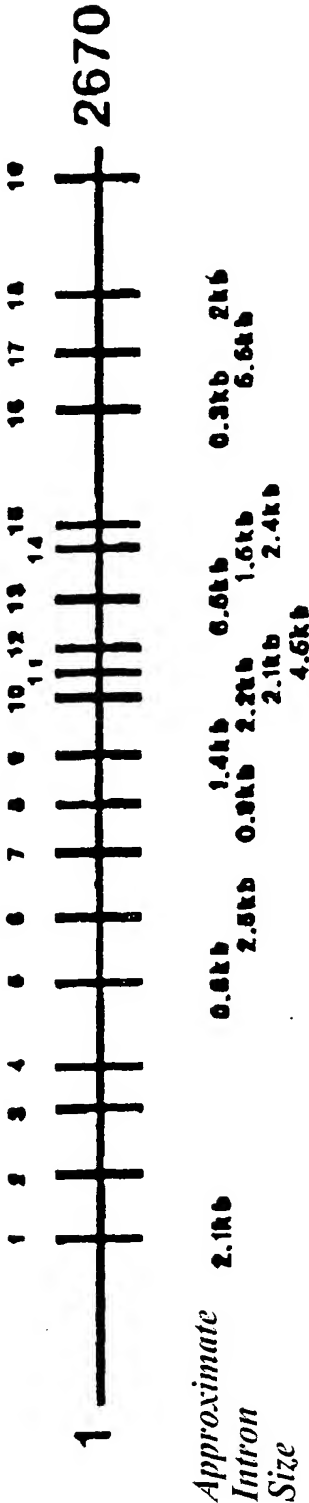


FIGURE 55A

10 20 30 40
 * * * * *
 CTC AAA AGG GGC CGG ATT TCC TTC TCC TGG AGG CAG ATG TTG CCT CTC

50 60 70 80 90
 * * * * * *
 TCT CTC GCT CGG ATT GGT TCA GTG CAC TCT AGA AAC ACT GCT GTG GTG

100 110 120 130 140
 * * * * * *
 GAG AAA CTG GAC CCC AGG GTG GTT TAT AAA ATC CTC CAA TGA AGC TAC

150 160 170 180 190
 * * * * * * *
 TAA CAT TAC TCC AAA GCA TAA TAT GAA AGC ATT TTT GGA TGA ATT GAA

Met Lys Ala Phe Leu Asp Glu Leu Lys>

200 210 220 230 240
 * * * * * * *
 AGC TGA GAA CAT CAA GAA GTT CTT ATA TAA TTT TAC ACA GAT ACC ACA

Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile Pro His>

FIGURE 55B

250 260 270 280
 * * * * * * *
 TTT AGC AGG AAC AGA ACA AAA CTT TCA GCT TGC AAA GCA AAT TCA ATC

Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile Gln Ser>

290 300 310 320 330
 * * * * * * *
 CCA GTG GAA AGA ATT TGG CCT GGA TTC TGT TGA GCT AGC ACA TTA TGA

Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His Tyr Asp>

340 350 360 370 380
 * * * * * * *
 TGT CCT GTT GTC CTA CCC AAA TAA GAC TCA TCC CAA CTA CAT CTC AAT

Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile Ser Ile>

390 400 410 420 430
 * * * * * * *
 AAT TAA TGA AGA TGG AAA TGA GAT TTT CAA CAC ATC ATT ATT TGA ACC

Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro>

440 450 460 470 480
 * * * * * * *
 ACC TCC TCC AGG ATA TGA AAA TGT TTC GGA TAT TGT ACC ACC TTT CAG

Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser>

FIGURE 55C

490 500 510 520
 * * * * * *
 TGC TTT CTC TCC TCA AGG AAT GCC AGA GGG CGA TCT AGT GTA TGT TAA

 Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn>

 530 540 550 560 570
 * * * * * * *
 CTA TGC ACG AAC TGA AGA CTT CTT TAA ATT GGA ACG GGA CAT GAA AAT

 Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile>

 580 590 600 610 620
 * * * * * * *
 CAA TTG CTC TGG GAA AAT TGT AAT TGC CAG ATA TGG GAA AGT TTT CAG

 Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg>

 630 640 650 660 670
 * * * * * * *
 AGG AAA TAA GGT TAA AAA TGC CCA GCT GGC AGG GGC CAA AGG AGT CAT

 Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly Val Ile>

 680 690 700 710 720
 * * * * * * *
 TCT CTA CTC CGA CCC TGC TGA CTA CTT TGC TCC TGG GGT GAA GTC CTA

 Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys Ser Tyr>

FIGURE 55D

730 740 750 760
 * * * * * * *
 TCC AGA TGG TTG GAA TCT TCC TGG AGG TGG TGT CCA GCG TGG AAA TAT

Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly Asn Ile>

770 780 790 800 810
 * * * * * * * *
 CCT AAA TCT GAA TGG TGC AGG AGA CCC TCT CAC ACC AGG TTA CCC AGC

Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr Pro Ala>

820 830 840 850 860
 * * * * * * * *
 AAA TGA ATA TGC TTA TAG GCG TGG AAT TGC AGA GGC TGT TGG TCT TCC

Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly Leu Pro>

870 880 890 900 910
 * * * * * * * *
 AAG TAT TCC TGT TCA TCC AAT TGG ATA CTA TGA TGC ACA GAA GCT CCT

Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys Leu Leu>

920 930 940 950 960
 * * * * * * * *
 AGA AAA AAT GGG TGG CTC AGC ACC ACC AGA TAG CAG CTG GAG AGG AAG

Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg Gly Ser>

FIGURE 55E

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970 980 990 1000
* * * * *
TCT CAA AGT GCC CTA CAA TGT TGG ACC TGG CTT TAC TGG AAA CTT TTC

Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn Phe Ser>

1010 1020 1030 1040 1050
* * * * *
TAC ACA AAA AGT CAA GAT GCA CAT CCA CTC TAC CAA TGA AGT GAC AAG

Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val Thr Arg>

1060 1070 1080 1090 1100
* * * * *
AAT TTA CAA TGT GAT AGG TAC TCT CAG AGG AGC AGT GGA ACC AGA CAG

Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro Asp Arg>

1110 1120 1130 1140 1150
* * * * *
ATA TGT CAT TCT GGG AGG TCA CCG GGA CTC ATG GGT GTT TGG TGG TAT

Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly Gly Ile>

1160 1170 1180 1190 1200
* * * * *
TGA CCC TCA GAG TGG AGC AGC TGT TGT TCA TGA AAT TGT GAG GAG CTT

Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg Ser Phe>

1210 1220 1230 1240
* * * * *
TGG AAC ACT GAA AAA GGA AGG GTG GAG ACC TAG AAG AAC AAT TTT GTT

Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile Leu Phe>

FIGURE 55F

1250 1260 1270 1280 1290
 * * * * * * *
 TGC AAG CTG GGA TGC AGA AGA ATT TGG TCT TCT TGG TTC TAC TGA GTG

Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp>

1300 1310 1320 1330 1340
 * * * * * * *
 GGC AGA GGA GAA TTC AAG ACT CCT TCA AGA GCG TGG CGT GGC TTA TAT

Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile>

1350 1360 1370 1380 1390
 * * * * * * *
 TAA TGC TGA CTC ATC TAT AGA AGG AAA CTA CAC TCT GAG AGT TGA TTG

Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val Asp Cys>

1400 1410 1420 1430 1440
 * * * * * * *
 TAC ACC GCT GAT GTA CAG CTT GGT ACA CAA CCT AAC AAA AGA GCT GAA

Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu Leu Lys>

1450 1460 1470 1480
 * * * * * * *
 AAG CCC TGA TGA AGG CTT TGA AGG CAA ATC TCT TTA TGA AAG TTG GAC

Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser Trp Thr>

FIGURE 55G

1490 1500 1510 1520 1530
 * * * * * * *
 TAA AAA AAG TCC TTC CCC AGA GTT CAG TGG CAT GCC CAG GAT AAG CAA

 Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile Ser Lys>

 1540 1550 1560 1570 1580
 * * * * * * *
 ATT GGG ATC TGG AAA TGA TTT TGA GGT GTT CTT CCA ACG ACT TGG AAT

 Leu Glv Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu Gly Ile>

 1590 1600 1610 1620 1630
 * * * * * * *
 TGC TTC AGG CAG AGC ACG GTA TAC TAA AAA TTG GGA AAC AAA CAA ATT

 Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn Lys Phe>

 1640 1650 1660 1670 1680
 * * * * * * *
 CAG CGG CTA TCC ACT GTA TCA CAG TGT CTA TGA AAC ATA TGA GTT GGT

 Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu Leu Val>

 1690 1700 1710 1720
 * * * * * * *
 GGA AAA GTT TTA TGA TCC AAT GTT TAA ATA TCA CCT CAC TGT GGC CCA

 Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val Ala Gln>

FIGURE 55H

1730	1740	1750	1760	1770
*	*	*	*	*
GGT	TCG AGG AGG	GAT GGT GTT TGA	GCT AGC CAA TTC	CAT AGT GCT CCC
Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val Leu Pro>				
1780	1790	1800	1810	1820
*	*	*	*	*
TTT	TGA TTG TCG AGA	TTA TGC TGT AGT TTT	AAG AAA GTA TGC	TGA CAA
Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala Asp Lys>				
1830	1840	1850	1860	1870
*	*	*	*	*
AAT	CTA CAG TAT TTC	TAT GAA ACA TCC	ACA GGA AAT GAA	GAC ATA CAG
Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr Tyr Ser>				
1880	1890	1900	1910	1920
*	*	*	*	*
TGT	ATC ATT TGA TTC	ACT TTT TTC TGC	AGT AAA GAA TTT	TAC AGA AAT
Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr Glu Ile>				
1930	1940	1950	1960	
*	*	*	*	*
TGC	TTC CAA GTT CAG	TGA GAG ACT CCA	GGA CTT TGA CAA	AAG CAA CCC
Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser Asn Pro>				

FIGURE 55I

1970 1980 1990 2000 2010
 * * * * * * *
 AAT AGT ATT AAG AAT GAT GAA TGA TCA ACT CAT GTT TCT GGA AAG AGC

Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu Arg Ala>

2020 2030 2040 2050 2060
 * * * * * * *
 ATT TAT TGA TCC ATT AGG GTT ACC AGA CAG GCC TTT TTA TAG GCA TGT

Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg His Val>

2070 2080 2090 2100 2110
 * * * * * * *
 CAT CTA TGC TCC AAG CAG CCA CAA CAA GTA TGC AGG GGA GTC ATT CCC

Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe Pro>

2120 2130 2140 2150 2160
 * * * * * * *
 AGG AAT TTA TGA TGC TCT GTT TGA TAT TGA AAG CAA AGT GGA CCC TTC

Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp Pro Ser>

2170 2180 2190 2200
 * * * * * * *
 CAA GGC CTG GGG AGA AGT GAA GAG ACA GAT TTA TGT TGC AGC CTT CAC

Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala Phe Thr>

2210 2220 2230 2240 2250
 * * * * * * *
 AGT GCA GGC AGC TGC AGA GAC TTT GAG TGA AGT AGC CTA AGA GGA TTC

Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala

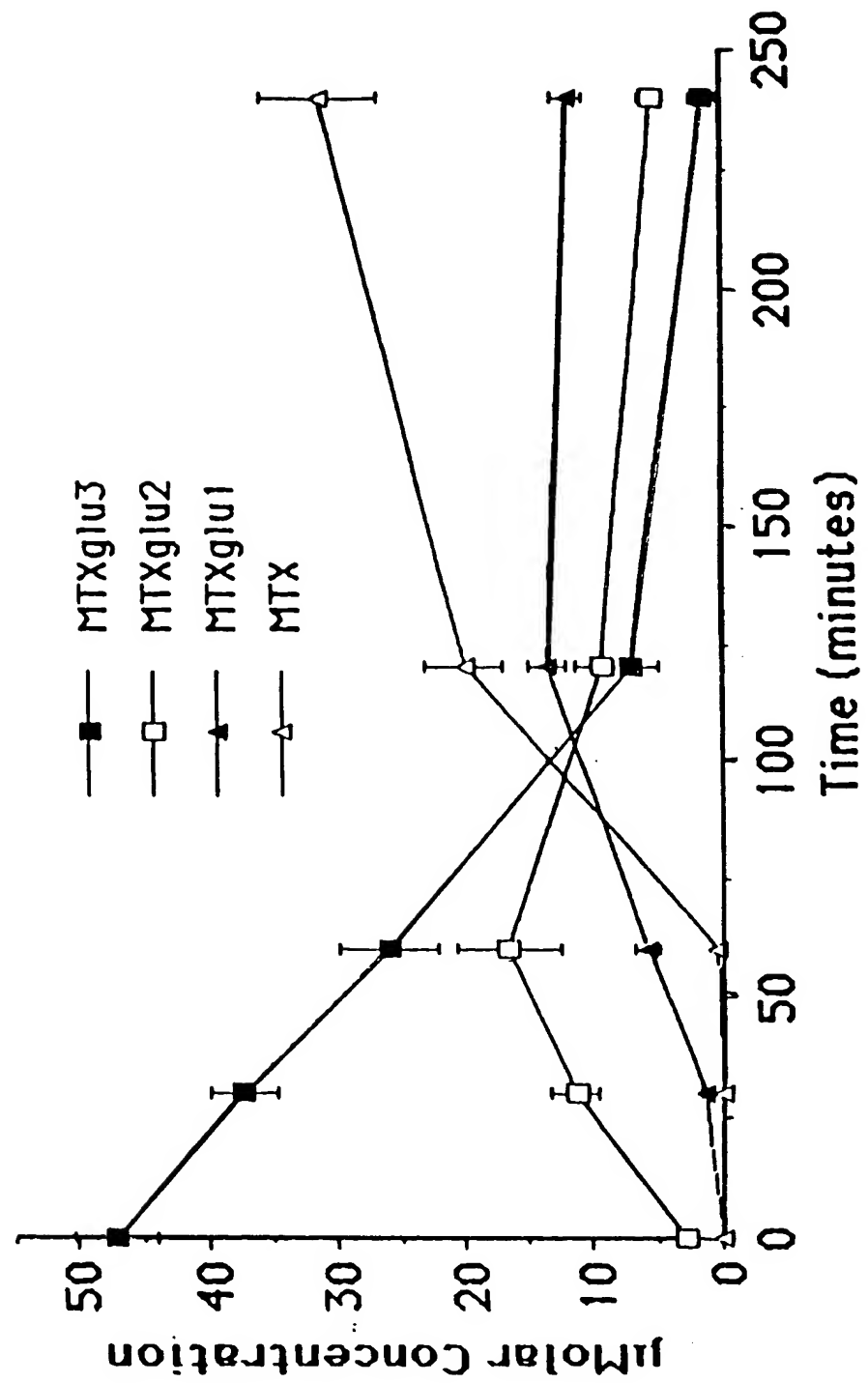
FIGURE 53J

2260 2270 2280 2290 2300
* * * * * *
TTT AGA GAA TCC GTA TTG AAT TTG TGT GGT ATG TCA CTC AGA AAG AAT

2310 2320 2330 2340 2350
* * * * * *
CGT AAT GGG TAT ATT GAT AAA TTT TAA AAT TGG TAT ATT TGA AAT AAA

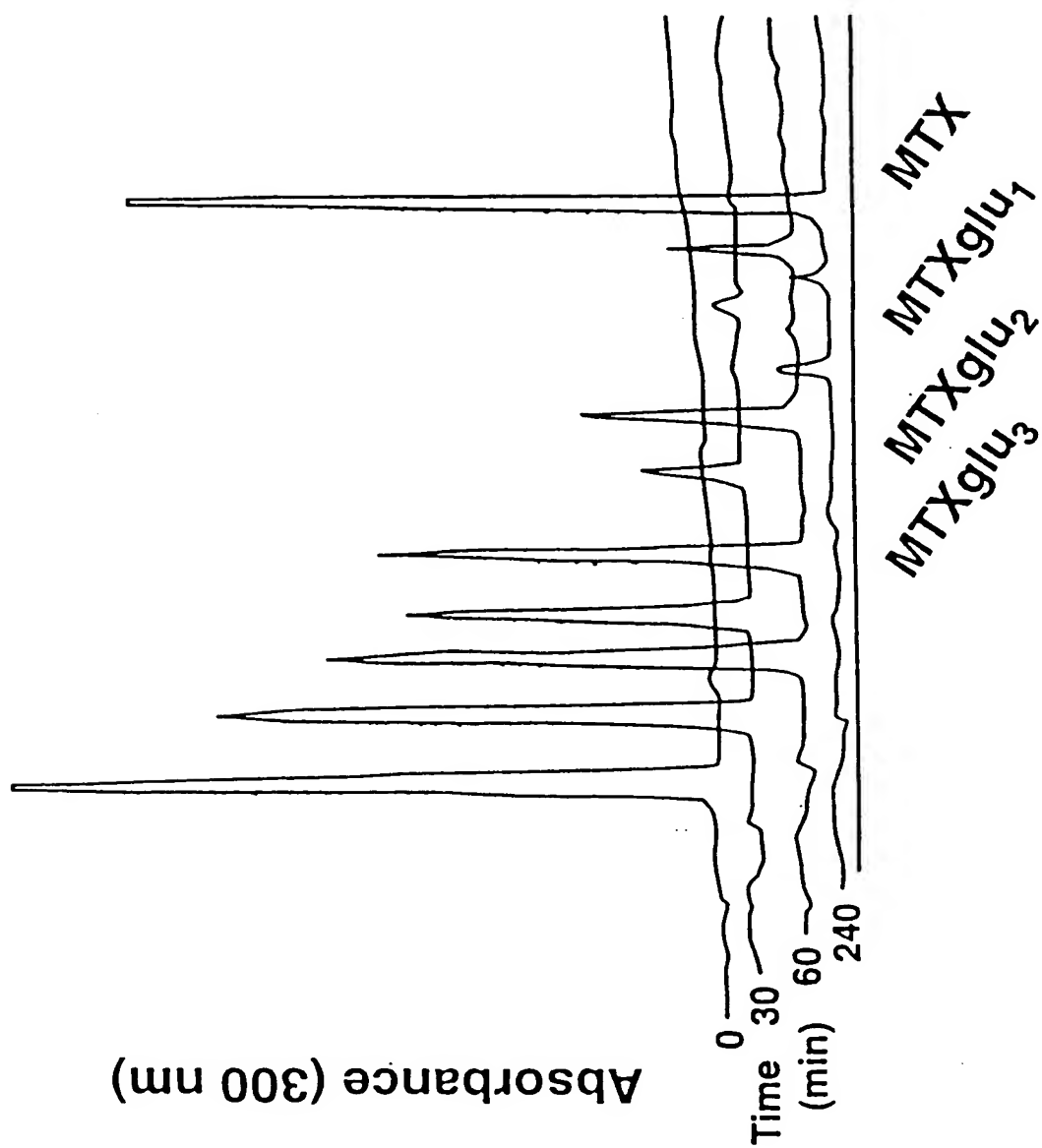
2360 2370 2380
* * * * *
GTT GAA TAT TAT ATA TAA AAA AAA AAA AAA AAA AA

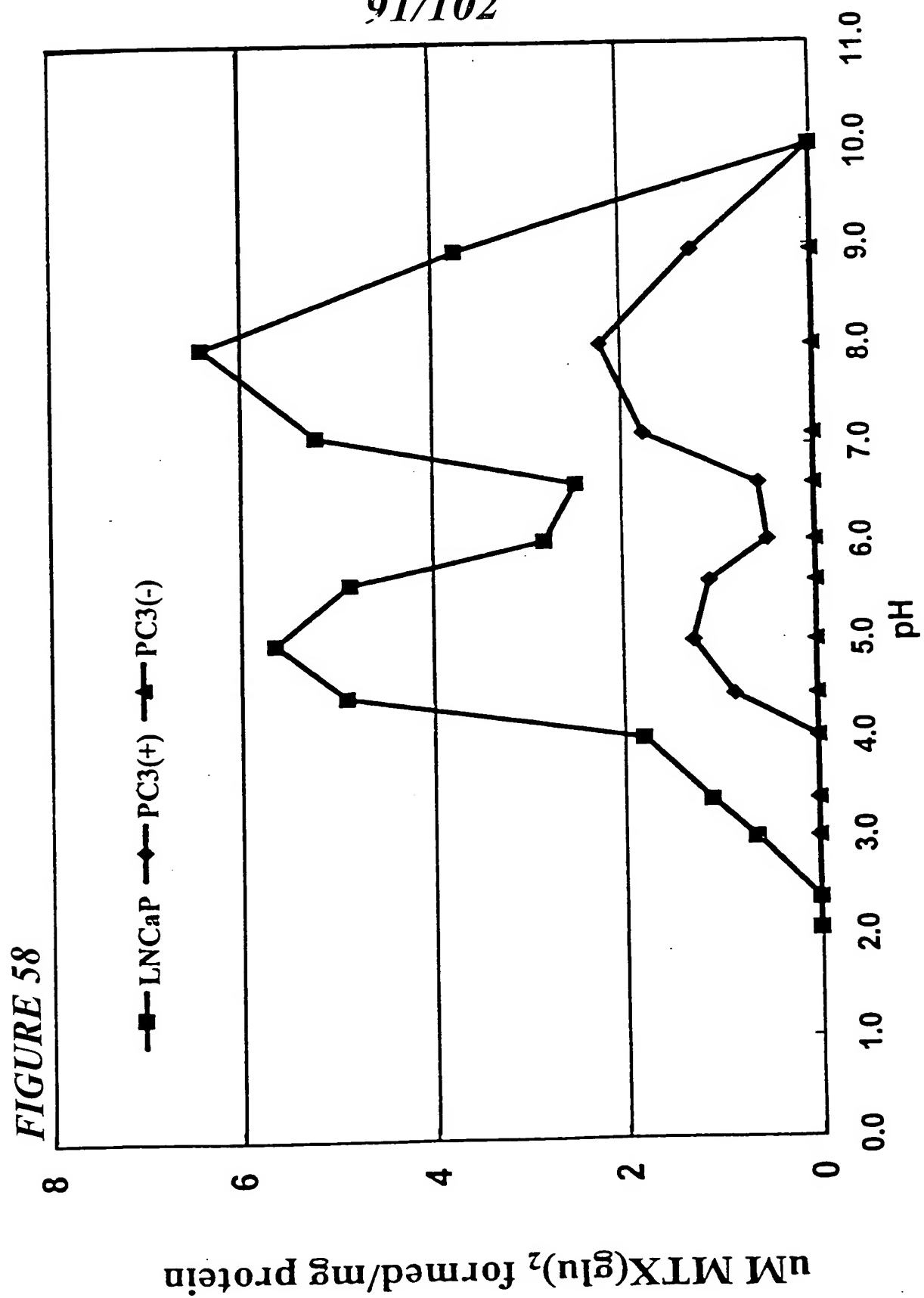
FIGURE 56

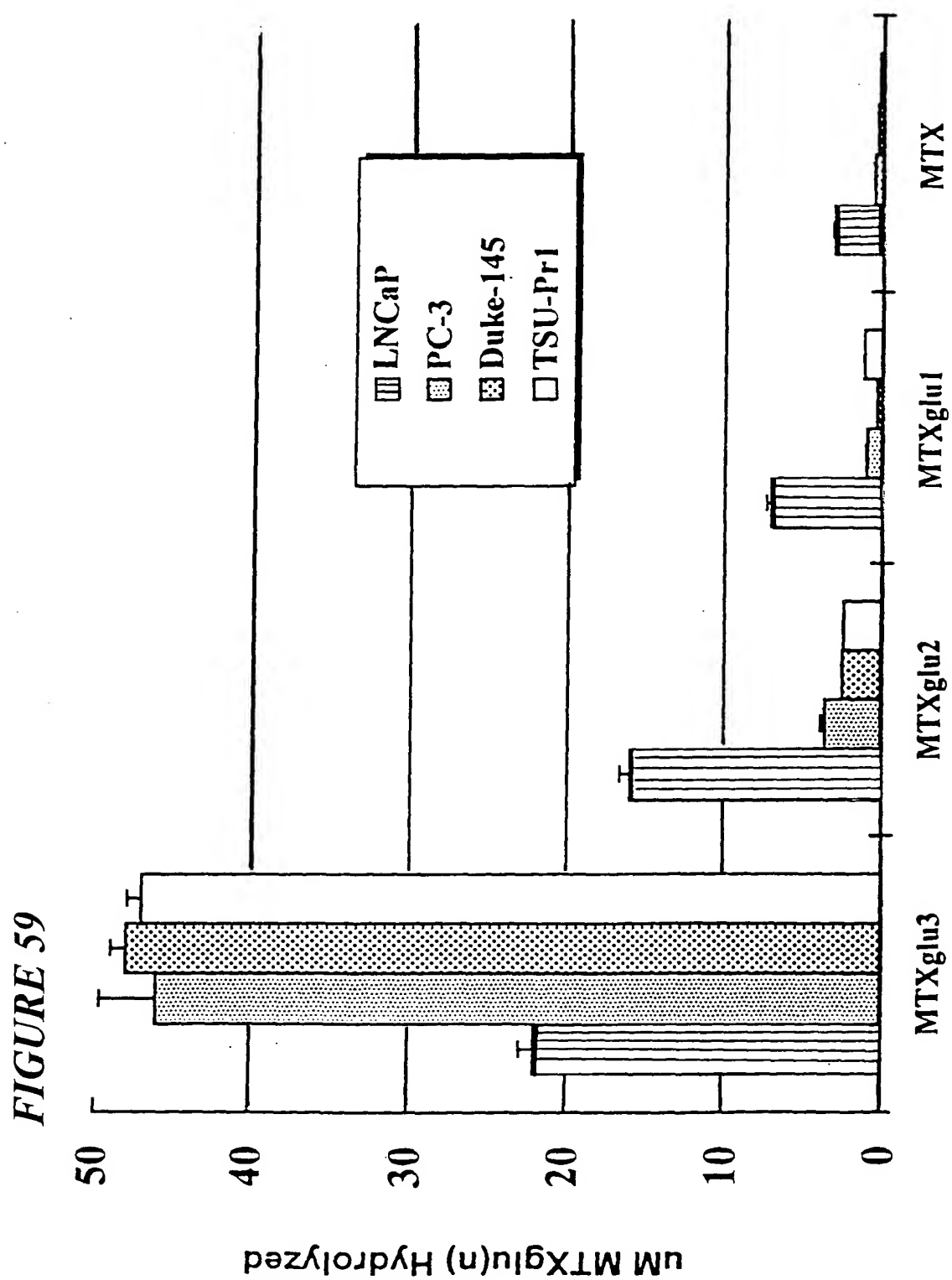


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FIGURE 57

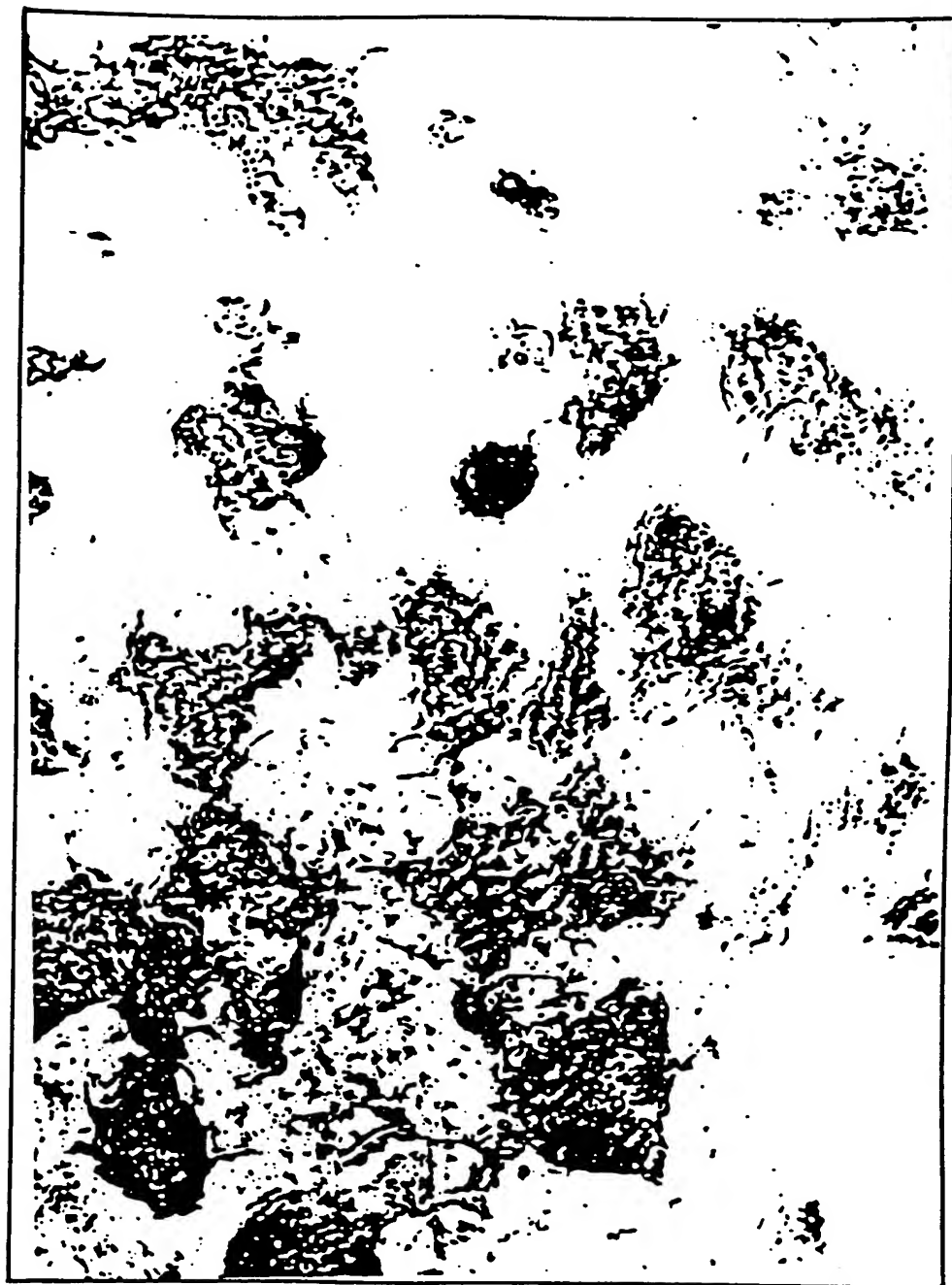






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FIGURE 60A



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FIGURE 60B



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FIGURE 60C

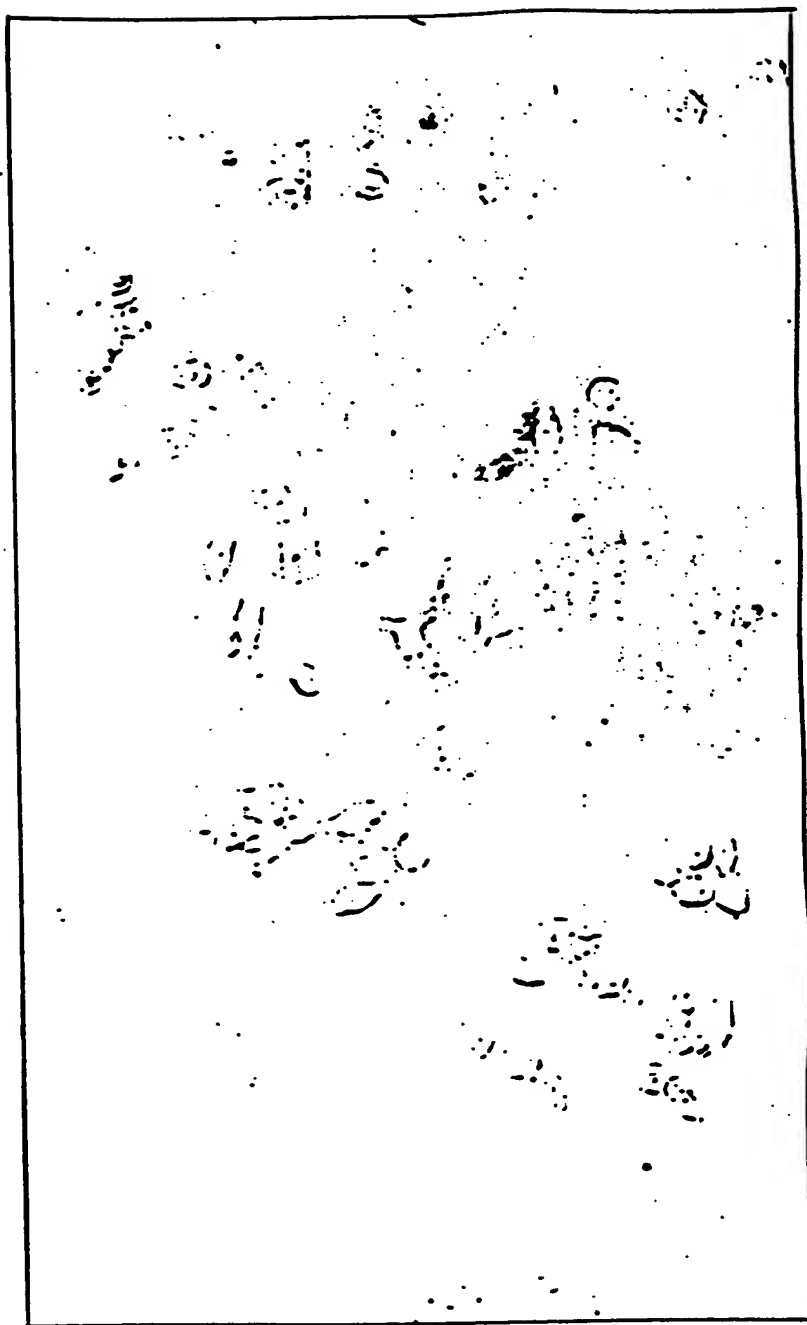


FIGURE 61

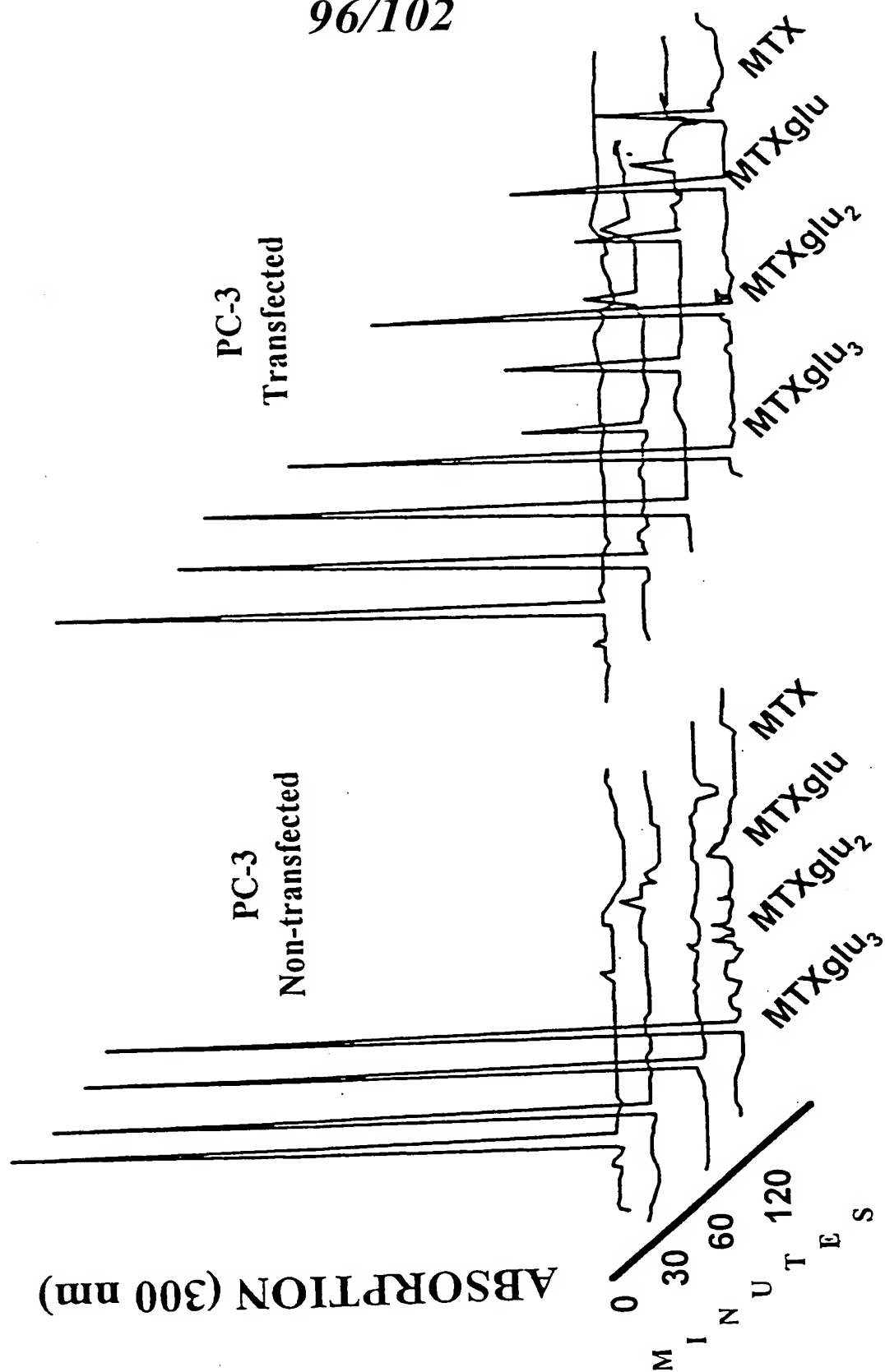


FIGURE 62

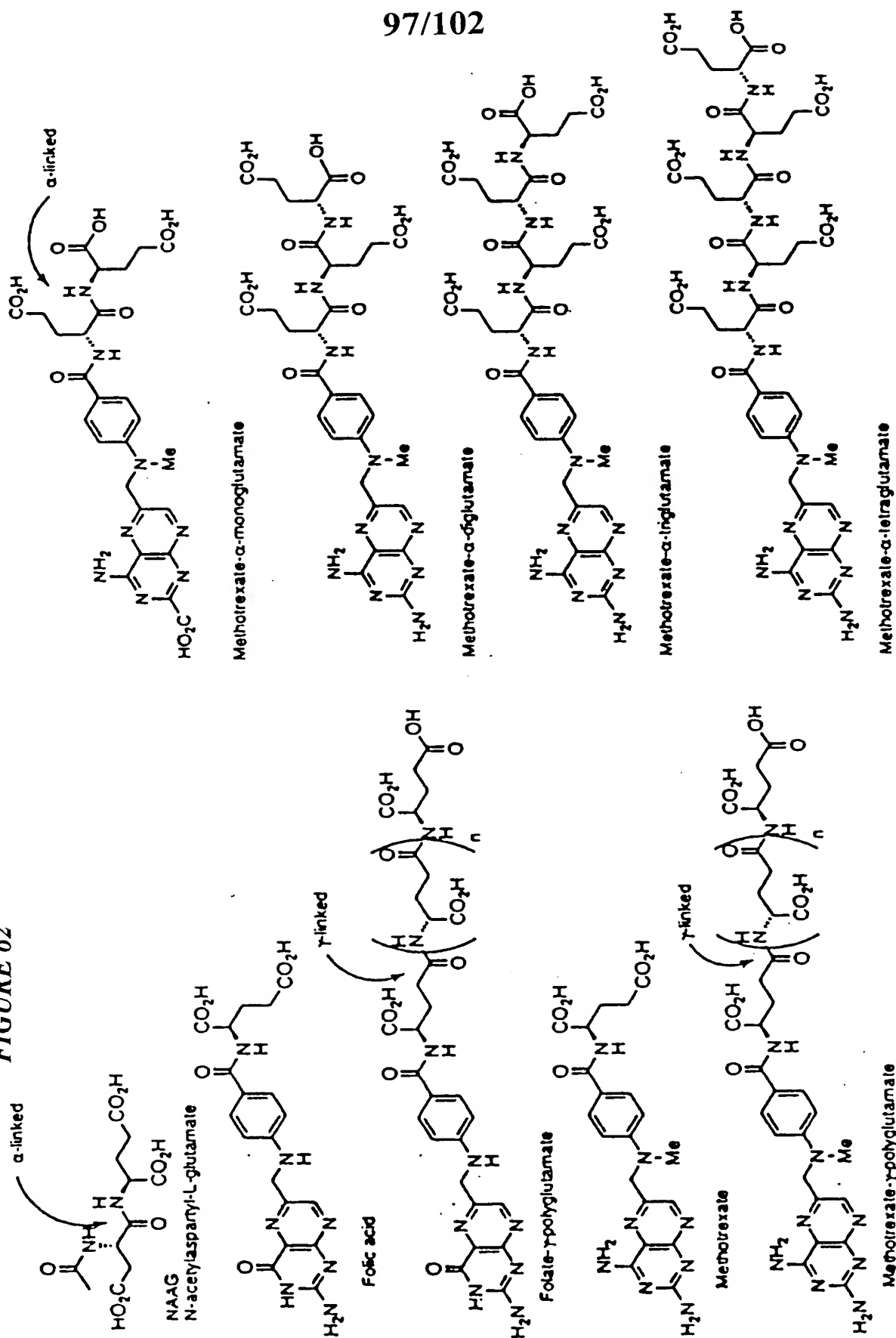


FIGURE 63A

Solid Phase Synthesis of Methotrexate α -polyglutamate Analogs

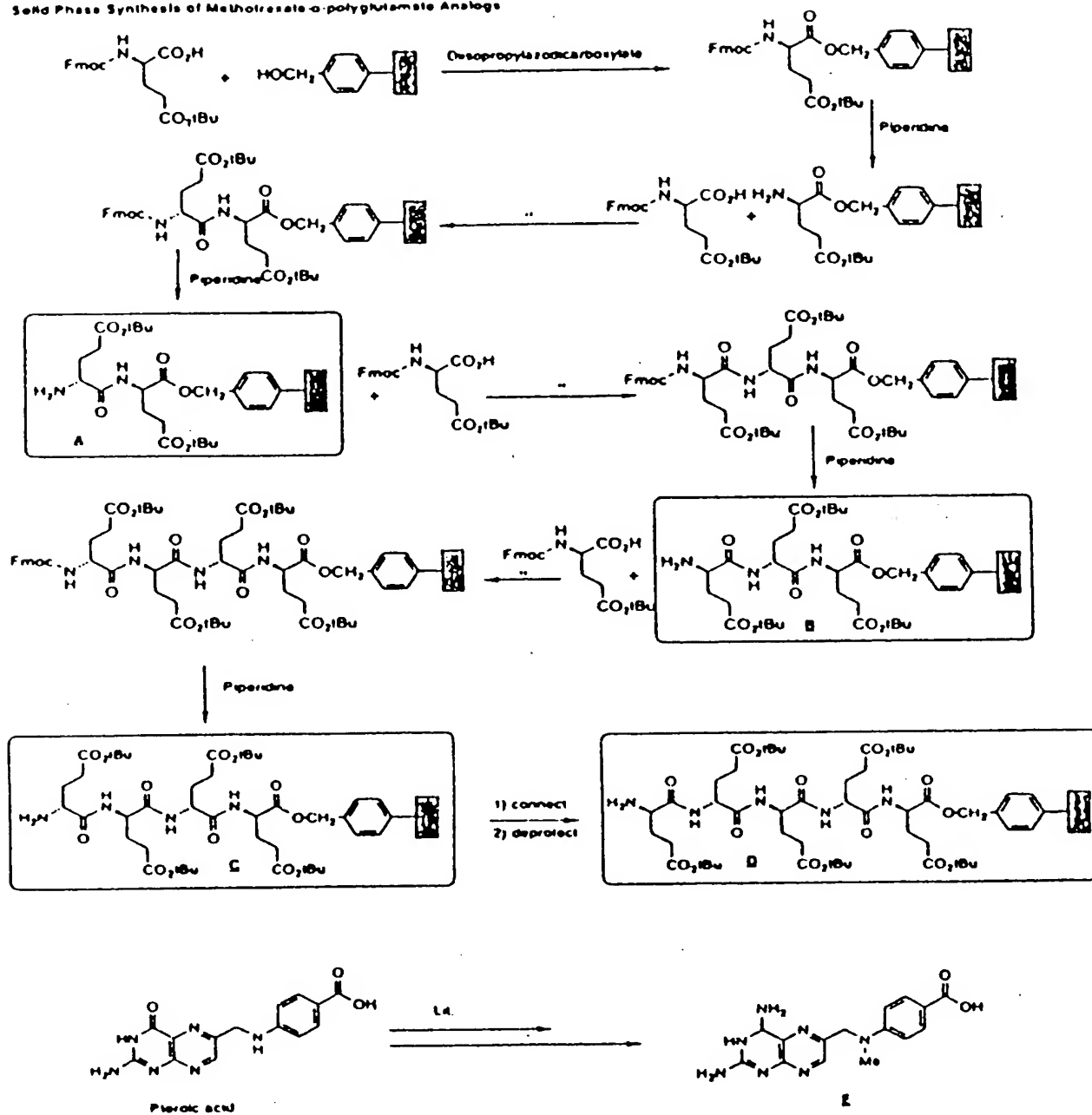


FIGURE 63B

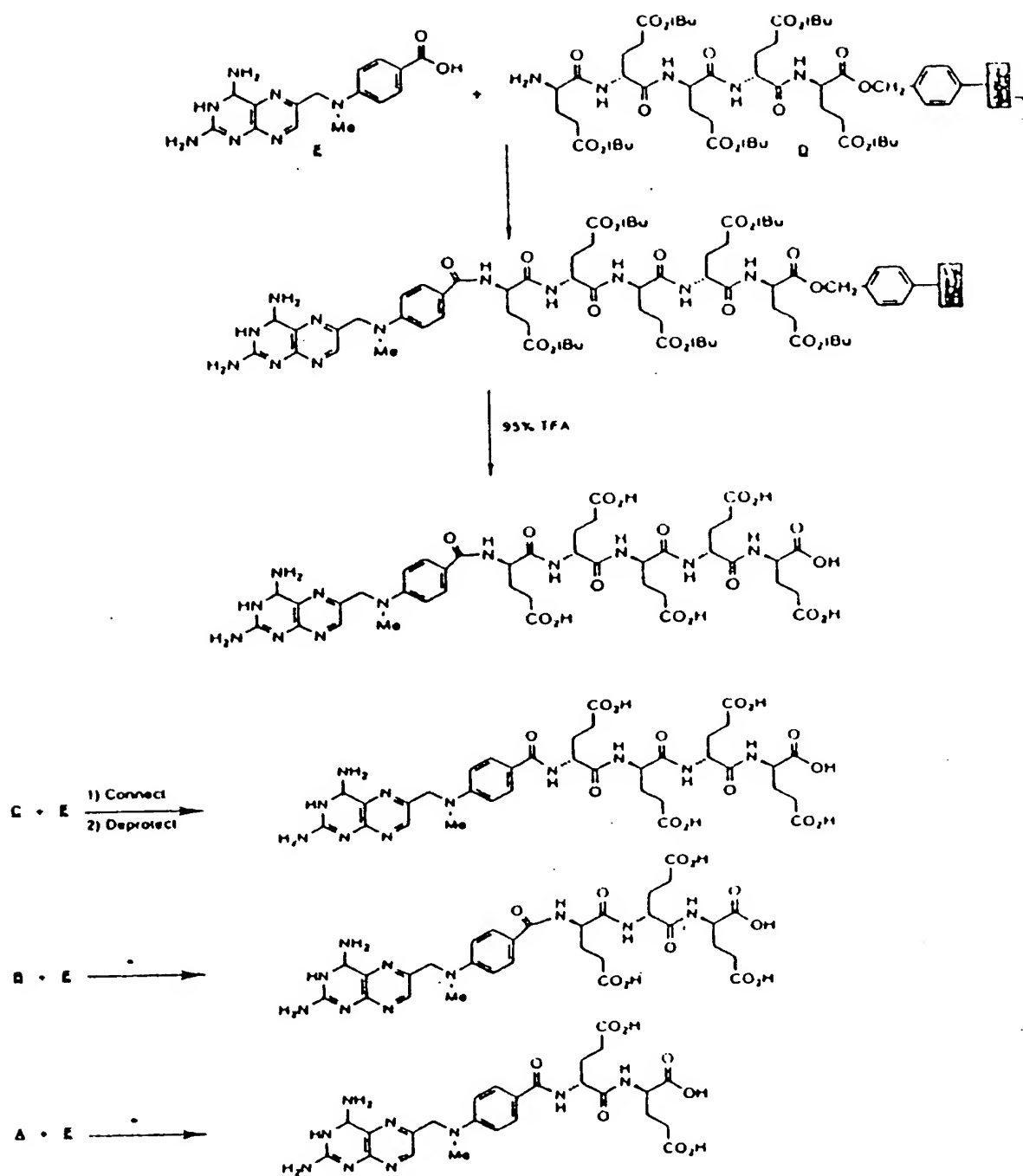


FIGURE 64

Sequence Analysis of microsatellite instability in PSM gene

<u>Sample</u>	<u>Sequence</u>	<u>PSM EXPRESSION (IMMUNO STAIN)</u>
Genomic	T ₉ GC(TTTTG) ₈ (TTTG) ₃ T ₇	
LNCaP	T ₉ GC(TTTTG) ₆ (TTTG) ₃ T ₇	positive
PC-3	T ₉ GC(TTTTG) ₈ (TTTG) ₃ T ₆	negative
DU145	T ₁₀ GC(TTTTG) ₅ (TTTG) ₂ T ₇	negative
T4 (tumor)	T ₁₀ GC(TTTTG) ₆ (TTTG) ₃ T ₇	positive
N4(paired normal)	T ₉ GC(TTTTG) ₆ (TTTG) ₃ T ₇	positive

FIGURE 65

Genomic Organization of PSM Gene

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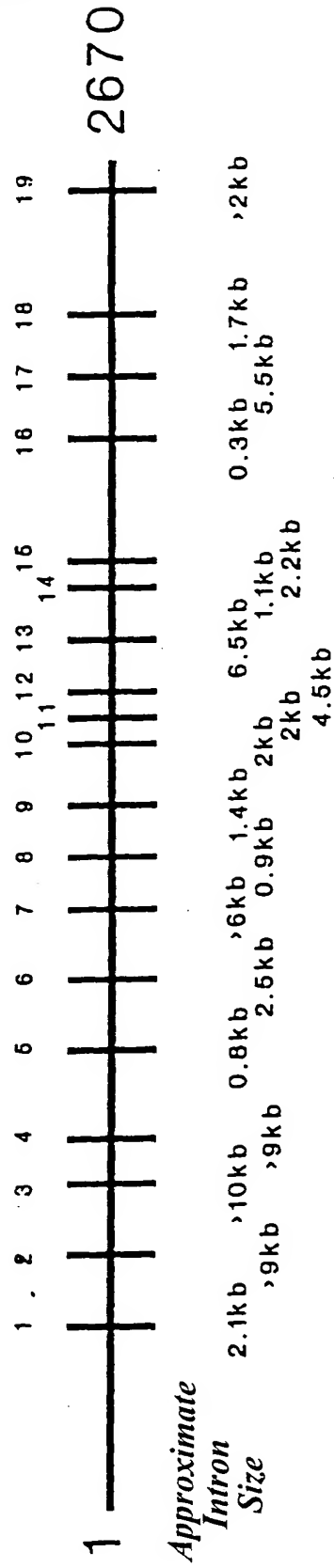


FIGURE 66

Location of microsatellite in PSM Gene

TTTTTTTTTGC(TTTTG)₆(TTTG)₃TTTTTTT

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